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January 21, 2006, 21:31:01; Search time 109 Seconds (without alignments) 3131.118 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                         1 aaagacggttatctggtgga......ccctttctaataaaagatgc 192
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/cgn2_6/ptodata1/ina/5_COMB.seq:*
/cgn2_6/ptodata1/ina/6A_COMB.seq:*
/cgn2_6/ptodata1/ina/6B_COMB.seq:*
/cgn2_6/ptodata1/ina/H_COMB.seq:*
/cgn2_6/ptodata1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata1/ina/PE_COMB.seq:*
/cgn2_6/ptodata1/ina/PE_COMB.seq:*
/cgn2_6/ptodata1/ina/PE_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1303057 seqs, 888780828 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                   US-10-721-793-115
192
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Maximum DB seq length: 2000000000
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| JUNEARM LITE OF SELISES.|
| JUNEARM LITE OF SELISES.|
| APPLICANT: GARCIA-RODRIGUEZ, Consuelo |
| APPLICANT: GARCIA-RODRIGUEZ, Consuelo |
| APPLICANT: CAMUNIO-ZUMIGA, Fernando |
| APPLICANT: BECERRIL-LUJAN, Baltazar |
| APPLICANT: POSSANI-POSTAY, Lourival D. |
| TITLE OF INVENTION: Primary Sequence and cDNA of |
| TITLE OF INVENTION: Insecticidally Effective Toxins from Scorpions of the |
| TITLE OF INVENTION: Genus Centruroides |
| TITLE OF INVENTION: Genus Centruroides |
| NUMBER OF SEQUENCES: 9 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Pinnegan, Henderson, Parabow, Garrett & ADDRESSEE: Dunner, L.L.P. |
| STREET: 1300 I Street, N.W. |
| COTY: Washington |
| COTY: Wash

ZIP: 20005
COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/053,021

USA

STATE: DC

NAME: Garret, Arthur S.
REGISTRATION NUMBER: 20,338
REFERENCE/DOCKET NUMBER: 06899.0001-01000
TELECOMMUNICATION INFORMATION:

(202) 408-4000

TELEPHONE:

TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 60/017,007
FILING DATE: 30-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/648,261
FILING DATE: 29-APR-1997
ATTORNEY/AGBNT INFORMATION:
NAME: Garrett, Arthur S.

Sequence 37, Appli Sequence 17726, A Sequence 17726, A Sequence 46727, A Sequence 16727, A Sequence 1285, Ap Sequence 1355, Ap Sequence 11751, A Sequence 11751, A Sequence 1670, A Sequence 1520, A Sequence 1520, A Sequence 1520, A Sequence 11, Appl Sequence 1, Appli Sequence 1, Appli Sequence 629, App Sequence 1, Appli Sequence 629, App Sequence 3, Appli Sequence 3, Appli Appli Appli Appli Sequence 3, Appli Sequence 8, Appli Sequence 8, A Sequence 11, Sequence 3 Description US-08-916-421B-1 US-09-692-570-1 US-09-692-570-1 US-09-830-230A-629 US-09-122-619-3 US-10-222-566-3 US-10-143-024A-3 US-09-949-016-17727 US-09-949-016-15170 US-09-949-016-16220 US-08-916-421B-1 US-09-692-570-1 US-09-053-021-3 US-09-053-021-8 US-09-599-632-11 SUMMARIES Match Length DB 345 3 243 3 1664976 1664976 16082 1664976 1664976 2591 40742 40747 1059 Query Score 121.4 121.4 Result Š 000

Sequence 1201, Ap Sequence 277, App Sequence 3441, Ap Sequence 3713, Ap Sequence 2713, Ap Sequence 5, Appli Sequence 5, Appli Sequence 40, Appl Sequence 213, App Sequence 213, App Sequence 659, App Sequence 783, App Sequence 270, App Sequence 783, App Sequence 783, App Sequence 783, App Sequence 270, App Sequence 270, App Sequence 783, App Sequence 783, App Sequence 270, App Sequence 270	
US-09-710-279-1201 US-09-134-001C-277 US-09-134-01C-277 US-09-134-001C-2351 US-09-134-001C-2351 US-09-134-001C-2351 US-09-134-001C-2351 US-09-146-803-5 US-09-246-786A-2701 US-09-246-786A-2701 US-09-248-786A-2701 US-09-248-786A-2701 US-09-248-786A-2701 US-09-248-786A-2701 US-09-276-594-002-659 US-09-976-594-002-659 US-09-978-978-971-9914 US-09-978-978-971-9914	US-09-781-8811-27 US-09-781-811-27 US-09-134-000C-1309 US-08-595-937A-1 US-08-447-185-3
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## ALIGNMENTS

US-09-053-021-3
; Sequence 3, Application US/09053021
; Patent No. 6270785
; GENERAL INFORMATION:

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160 TGCTACAAGCTTGCATGCTGGTGGAAGGTTTGCCCGAAAGTACACCGACTTATCCCATT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GAAAACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTAT 117
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Pred. No. 4.2e-31;
0; Mismatches 36;
                                                                                                                                             FILING DATE: 29-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: GARTECT, Arthur S.
REGISTRATION NUMBER: 20,338
REFERENCE/DOCKET NUMBER: 06899.0001-01000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09599632
; Sequence 11, Application US/09599632
; Patent No. 6768002
; GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Herrman, Rafael
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1375 US NA
CURRENT APPLICATION NUMBER: US/09/599,632
CURRENT FILING DATE: 2000-06-22
FRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
TYPE: DNA
                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,007
FILING DATE: 30-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/848,261
                                                                                                                                                                                                                                                                             TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.2%;
Best Local Similarity 80.0%;
Matches 156; Conservative
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; LOCATION:
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Sequence 8, Application US/09053021

Sequence 9, Application US/09053021

GENERAL INFORMATION:
APPLICANT: SELISKO, Barbara
APPLICANT: BECERIL-LUJAN, Baltazar
APPLICANT: BECERIL-LUJAN, Baltazar
APPLICANT: POSSANI-POSTAY, Lourival D.
TITLE OF INVENTION: Primary Sequence and cDNA of
Patent No. 6270785

TITLE OF INVENTION: Insecticidally Effective Toxins from Scorpions of the
TITLE OF INVENTION: Genus Centruroides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GAAAACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTAT 117
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Pred. No. 4e-31;
0; Mismatches 36; Indels 3
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ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,021
                                                                               MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Centruroides noxius Hoffman
DEVELOPMENTAL STAGE: Adult
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.2%;
80.0%;
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LENGTH: 301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0°
Matches 156; Conservative
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40..243
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                                                                                                                                                                                             LIBRARY: CDNA
CLONE: CngtVIII
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NAME/KEY:
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FEATURE:
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LOCATION:

US-09-053-021-3
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OTHER INFORMATION: n equals a, t,
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LOCATION: (600992)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (657081). (657081)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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OCHER INFORMATION: n equals a, t, MAME/KEY: misc_feature
LOCATION: (674435). (674435)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (682442). (682442)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (13652). (713652)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (713652). (713652). OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
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LOCATION: (312993). (312993)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
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NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234520)..(234220)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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ION: (312837)..(312837)
INFORMATION: n equals a,
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INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
NAME/KEY: misc.feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
                                                                                                    NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a,
                                                                                                                                                           /KBY: misc feature
FION: (231980)..(231980)
R INFORMATION: n equals a,
                 CCATION: (163385)..(163385)
THER INFORMATION: n equals a,
                                                   /KBY: misc feature
IION: (191989)..(191989)
R INFORMATION: n equals a,
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FION: (234187)..(234187)
? INFORMATION: n equals a,
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                                                                                            Gaps
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                                                                                                                                                                                                   137 ATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCTAATAAAAGATG 191
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                                                      Query Match 18.2%; Score 35; DB 3; Length 243; Best Local Similarity 56.5%; Pred. No. 0.051; Matches 65; Conservative 0; Mismatches 50; Indels
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LOCATION: (84773)..(84713)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
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LOCATION: (28222). (28222)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (28257). (28258)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
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LOCATION: (98256)..(98266)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
, ORGANISM: Hottentotta judaica
US-09-599-632-11
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CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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LENGTH: 1664976
LENGTH: 10 DNA
ORGANISM: Methanococcus jannaschii
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t,
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Sequence 1, Application US/09692570

Sequence 1, Application US/09692570

Sequence 1, Application US/09692570

Sequence 1, Application US/09692570

GENERAL INFORMATION:

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: januaschii

FILE REPERENCE: PB275C1

CURRENT APPLICATION NUMBER: US/09/692,570
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; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1084830)
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LOCATION: (1119881)..(1119881)
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LOCATION: (113081)..(1130881)
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LOCATION: (713552)..(713652)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t,
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t,
                                                                                                                      NAME/KEY: misc feature
LOCATION: (234220)...(234220)
OTHER INFORMATION: n equals a, t,
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LOCATION: (600992)..(600992)
YTHER INFORMATION: n equals a, t,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t,
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LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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LOCATION: (682442)...(682442)
OTHER INFORMATION: n equals a,
                  OTHER INFORMATION: n equals a, PEATURE:
NAME/KEY: misc_feature
LOCATION: (234187). (234187)
OTHER INFORMATION: n equals a, PEATURE:
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a,
ION: (231980)..(231980)
INFORMATION: n equals a,
                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (234814)...(234814)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
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LOCATION: (559167)...(559167)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
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210409 AIACAGITIGIGGGATTAACAAGCTIACCTGCAAGITIAAIAGCTGGAIATTIGTGGAAGA 210468
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18.2%; Score 35; DB 3; Length 1664976;
Best Local Similarity 56.5%; Pred. No. 1.7;
Matches 65; Conservative 0; Mismatches 50; Indels 0;
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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Patent No. 6902893

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Lyme Disease Vaccines

FILE REFRENCE: P8481US
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c,
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NAME/KEY: misc_feature
LOCATION: (1313224)...(1313224)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (1084830). (1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (871619)...(871619)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
FRATURE:
NAMB/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals
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US-09-830-230A-629
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4039 GGGATGAAGAAGGATGATCAGATTGCTGCTGTTTGCTTTGAGGGGGATGGCTAAGGAT 4098
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Patent No. 6719983

GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARBHAM, JOHN M.
APPLICANT: HARBHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: WEINSTOCK, GEORGE M.
FILE REFERENCE: UTSH.2344503
CURRENT FILING DATE: 2002-08-16
FULR REFERENCE: UTSH.2344503
FULR APPLICATION NUMBER: 09/125,619
PRIOR PILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGH: 7766
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APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
TILLE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH, 7766
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Pred. No. 1.5;
0; Mismatches 56; Indels 0
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                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Borrelia burgdorferi
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Best Local Similarity 54.1%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                  LOCATION: (127)
OTHER INFORMATION: R = A OR
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Matches 66; Conservative
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NAME/KEY: misc feature
LOCATION: (1251)
OTHER INFORMATION: n equals a,t,g, or c
US-09-830-230A-629
           PRIOR APPLICATION NUMBER: 60/053,344
PRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR FILING DATE: 1997-07-22
PRIOR FILING DATE: 1997-07-22
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 756
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 3990
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Patent No. 6437116
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRIXN K.
APPLICANT: BARBOUR, ALAN G.
                                                                                                                                                                                                                                                                                                                         LOCATION: (1139)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (1143)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (1210)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (1244)
OTHER INFORMATION: n equals a,t,9,
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                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (1139)
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LOCATION: (1250)
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                                                                                                                                                                                                                                     TYPE: DNA
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PRIOR FILING DATE: 1999-01-27
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US-09-949-016-17726
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    1039 GGGATGAAGAAGGATGATCAGATTGCTGCTGCTATTGCTTTGAGGGGGATGGCTAAGGAT 4098
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                                                                                                                                                                  Sequence 3, Application US/10143024A
; Sequence 3, Application US/10143024A
; Patent No. 6740744
; GENERAL INFORMATION:
APPLICANT: JUNCA-REN, ZHANG
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMD-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FULR REFERENCE: UTSH: 234 USD1
CURRENT FILING DATE: 2002-08-23
FRIOR FILING DATE: 1999-01-27
FRIOR PILING DATE: 1999-01-27
FRIOR PILING DATE: 1997-02-20
FRIOR PILING DATE: 1997-02-20
FRIOR PILING DATE: 1997-02-20
FRIOR PILING DATE: 1997-02-21
FRIOR PILING DATE: 1997-02-21
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOYCK, GEORGE M.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VWP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Indels
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CURRENT FILING DATE: 2002-08-16
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Patent No. 6878816
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: R = A OR G
US-10-143-024A-3
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Best Local Similarity 54.1%;
Matches 66; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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RESULT 11

US-09-49-016-17726/c

J Gequence 17726, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT PILLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 17726
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Pred. No. 1.5;
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Pred. No. 0.75;
0; Mismatches
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                                                                                                     TYPE: DNA
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                           16.9%;
54.1%;
                                                                                                                                                                        ; NAWE/KEY: modified_base; LOCATION: (127); OTHER INFORMATION: R = A OR US-10-222-162-3
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Best Local Similarity 54.14
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.7
Best Local Similarity 52.2
Matches 71; Conservative
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 7766
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us-10-721-793-115.rni

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Sequence 46727, Application US/09949016
; Sequence 46727, Application US/09949016
; Patent No. 681239
; GRMERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION: WIMBER: 60/241,755
   PRIOR PPLICATION NUMBER: 60/241,755
   PRIOR PLLING DATE: 2000-10-20
   PRIOR PLLING DATE: 2000-10-03
   PRIOR PLLING DATE: 2000-10-08
   NUMBER OF SEQ ID NOS: 207012
   SOFTWARE: PRESESEQ for Windows Version 4.0
   SEQ ID NO 46727
   LENGTH: 601
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; Sequence 1285, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
    APPLICANT: Cocks, Benjamin G.
    APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Schlhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
; CORRESPONDENCE ALTO
    STATE: CALIFORNIA

COUNTRY: USA
                            98 GAGGAGGTAATTACGGCTATTGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATA 157
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                                                                                38 ACACTTGCTGGATATTGGGAGAAAAAAAATACTGCAATAGGGAATGCACATGGAAGCACC
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Pred. No. 0.75,
0; Mismatches
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COMPUTER READABLE FORM:
WEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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52.2%;
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Best Local Similarity 52.2.
Best Local 71; Conservative
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US-09-949-016-46727/c
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US-09-949-016-46727
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        Sequence 17727, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR PELING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 17727
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Sequence 46726, Application US/09949016

Sequence 46726, Application US/09949016

Sequence 46726, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ATTILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILER REPRENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PLILOR DATE: 2000-10-20

PRIOR PLILOR DATE: 2000-10-20

PRIOR PLILOR DATE: 2000-10-03

PRIOR PLILOR DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 46726

LENGTH: 601
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16.7%; Score 32; DB 3; Length 601;
Best Local Similarity 52.2%; Pred. No. 0.75;
Matches 71; Conservative 0; Mismatches 65; Indels
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52.2%; Pred. No. 0.75;
ive 0; Mismatches 65; Indels
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Best Local Similarity 52.2
Matches 71; Conservative
US-09-949-016-17727/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17727
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ORGANISM: Human
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0001 US
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION
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Sequence Sequence Sequence

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US-10-829-826B-71
US-10-829-826B-65
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US-10-829-826B-87
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US-10-829-826B-71
US-10-829-826B-79
US-10-829-826B-79
US-10-829-826B-83

Sequence Sequence Sequence

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ALIGNMENTS

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778 CITAAAAAACAATIGATCATIGITAAAAGAAGGAAAATACICAAAITICAATITIGCAIG 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ## Sequence 56579, Application US/10750185

## Sequence 56579, Application US/10750185

## Publication NO. US2005026063A1

## GENERAL INFORMATION:
## APPLICANT: MAI GENOMICS, INC.
## APPLICANT: KERR, Richard
## APPLICANT: ROSNFELD, David
## APPLICANT: BATES, Stephen
## APPLICANT: BATES, Stephen
## APPLICANT: PANTIN, Dennis
## TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
## TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
## CURRENT PRILING DATE: 2003-12-31
## PRIOR PELING DATE: 2003-12-31
## PRIOR PILING DATE: 2003-12-31
## PRIOR PILING DATE: 2003-12-31
## PRIOR PILING DATE: 2003-12-31
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16.0%; Score 30.8; DB 7; Length 34
Best Local Similarity 52.3%; Pred. No. 1;
Matches 68; Conservative 0; Mismatches 62; Indels
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US-10-750-185-56579
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SOFTWARE: Patentin version 3.1
SEQ ID NO 56579
LENGTH: 3493
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US-10-750-623-56579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56579, A
Sequence 56579, A
                                                                                                    ; Search time 224 Seconds (without alignments) 706.520 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq3:*
               GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-10-750-185-52777

US-10-750-623-52777

US-10-790-623-31353

US-10-790-623-31353

US-10-750-185-31353

US-10-750-185-31353

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US-10-829-826B-46
US-10-829-826B-56
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Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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DB 7; Length 3493;

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                                                                                                                                                                                                                                                         Sequence 3441, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE REPERENCE: PUJ4860US
FILE REPERENCE: PUJ4860US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3441
LENGTH: 3153
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APPLICANT: MIG GENOMICS, INC.
APPLICANT: BOSINEE, Side K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
SHOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PARENTIN VEREION 3.1
SEQ ID NO 52777
LENGTH: 2515
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15.7%; Score 30.2; DB 7; Length 3153;
Best Local Similarity 52.8%; Pred. No. 1.6;
Matches 65; Conservative 0; Mismatches 58; Indels 0
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Publication No. US20050260603A1
GENERAL INFORMATION:
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; ORGANISM: Bovine 19866880359186
US-10-750-185-52777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                   149 TGT 151
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US-10-793-626-3441/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1201
LENGTH: 1100
                                                                        APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENER.
APPLICANT: REER, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN. Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOD.
CURRENT FILING DATE: 2003-12-31
FAIOR APPLICATION NUMBER: US 60/437,482
FRIOR FILING DATE: 2002-12-31
FRIOR FILING DATE: 2002-12-31
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 56579
LENGTH: 3493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.0%; Score 30.8; DB 7; Length 3493; 52.3%; Pred. No. 1; ive 0; Mismatches 62; Indels 0
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Sequence 56579, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1201, Application US/10793626; Publication No. US20050255478A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Bovine 19866880937875
US-10-750-623-56579
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Matches 68; Conserv
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                                                                                                                            121 agarartricriciggradgaaaagcrgrgaaggaggrrcaaggrcagaargrrgagaagaaa 180
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU348002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3532
LENGTH: 4103
                                                                                   3 AGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAAAA
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                                               Gaps
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: MEINER, Sue K.
APPLICANT: KERN, Richer, Baré
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Sue M.
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
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Score 29.8; DB 7; Length 2515; Pred. No. 2; 0; Mismatches 32; Indels 0
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Pred. No. 2;
0; Mismatches 32;
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PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 52777
LENGTH: 2515
                                                                                                                                                                                                                                                                                                                   Sequence 52777, Application US/10750623
Publication No. US20050287531A1
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Sequence 3532, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:
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                                                                                                                                                                                                              181 ATCATTCTGCTATAAGCAATG 201
                                                                                                                                                                       63 CAAATACTGCAATAGGGAATG 83
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US-10-750-623-52777
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      Query Match
Best Local Similarity 60.5%;
Matches 49; Conservative
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Best Local Similarity 60.5%;
Matches 49; Conservative
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Sequence 3529, Application US/10793626
Sequence 3529, Application No. US20050255478A1
GENERAL INFORMATION:
APPLICAPT KIMMERINY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TILLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2044-03-04
CURRENT FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 3629
LENGTH: 3394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
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APPLICANT: BATES, Sephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Indels
                                                                                                                                  69; Indels
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                                                                                   DB 7;
                                                                                Score 29.6; DI
Pred. No. 2.9;
0; Mismatches
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; OTHER INFORMATION: nucleic acid sequence US-10-793-626-3532
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                                                                                                                                                                                                                                                                                                                                                                                                                                   4083 ATTTGAAAAATGATAGATG 4102
                                                                                                                                                                                                                                                                                                                                                                                       172 CCCCTTTCTAATAAAGATG 191
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ORGANISM: Artificial Sequence
                                                                                   Query Match
Best Local Similarity 50.7%;
Matches 71; Conservative
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.3%
Local 61; Conservative
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US-10-793-626-3629/c
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US-10-750-185-31353
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US-10-750-623-41036
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APPLICANT: MAI GENOMICS, INC.

APPLICANT: DeNISE, Sue K.

APPLICANT: DENISE, Sue K.

APPLICANT: RESENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: RAFEN, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMILLOO-1

CURRENT APPLICATION NUMBER: US 6/437,482

FRIOR APPLICATION NUMBER: 2003-12-31

PRIOR FILING DATE: 2002-12-31

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PATCHIN VERSION 3.1
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                                                                                                                                                                                    Query Match
15.1%; Score 29; DB 7; Length 1232;
Best Local Similarity 58.8%; Pred. No. 2.9;
Matches 50; Conservative 0; Mismatches 35; Indels
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Publication No. US20050287531A1
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: MOSENVELD, David
                                                                                                    TYPE: DNA
ORGANISM: Bovine 19866880618861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine 19866880618861
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 31353
LENGTH: 1232
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BATES, Stephen
FANTIN, Dennis
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US-10-750-185-41036
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1242 TTGCCTGGGAAATCAGTGGGGTTGCAAAGAGTCAGACGTGACTTGGCAACTAAACAACAA 1301
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; Publication No. US20050287531A1
; GENERAL INFORMATION:
    APPLICANT: MMI GENOMICS, INC.
    APPLICANT: RERR, Richard
    APPLICANT: RERR, Richard
    APPLICANT: ROSENFELD, David
    APPLICANT: BATES, Stephen
    APPLICANT: BATES, Stephen
    APPLICANT: BATES, Stephen
    APPLICANT: MAININ, Dennis
    TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
    FILE REFERENCE: MMI1100-1
    CURRENT PILING DATE: 2003-12-31
    PRIOR FILING DATE: 2002-12-31
    PRIOR FILING DATE: 2002-12-31
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VETRION 3.1
SEQ ID NO 41036
LENGTH: 1764
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                                                                                                                                                                                                                                                                                                                               , ORGANISM: Bovine 19866881141918
US-10-750-185-41036
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SOFTWARE: Patentin version 3.1
SEQ ID NO 41036
LENGTH: 1764
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Best Local Similarity 54.81
Matches 57; Conservative
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| Sequence 3-64669, Application US/10750623
| Publication No. US20050287531A1
| GENERAL INFORMATION:
| APPLICANT: PMI GENOMICS, INC.
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: PATTIN, Dennis
| APPLICANT: PATTIN, Dennis
| APPLICANT: PATTIN BETHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
| FILE REPERENCE: MAILION-1
| CURRENT PILING DATE: 2003-12-31
| CURRENT PILING DATE: 2003-12-31
| PRIOR FILING DATE: 2002-12-31
| NUMBER OF SEQ ID NOS: 64922
| SEQ ID NO 54668
| LENGTH: 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                           APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIJ100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: 05 60/437,482
SQUID NOS: 64922
SOFTWARE: PARENTIN VERSION 3.1
SQUID NO 54668
LENGTH: 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.6%; Pred. No. 5;
Matches 45; Conservative 0; Mismatches 28; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1002;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.2; DB 7; Length 1 Pred. No. 5; 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Bovine 19866880898655
US-10-750-185-54668
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US-10-750-623-54668
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Best Local Similarity 61.6%;
Matches 45; Conservative
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KERR, Richard
ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 CTATTGCGAAGGA 147
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                     APPLICANT:
APPLICANT:
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US-10-750-185-57766

RESULT 15

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January 21, 2006, 21:31:18; Search time 2178 Seconds (without alignments) 728.981 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USOBA_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USOBA_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USOBA_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USOBB_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USOBB_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOBB_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOBB_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USOBB_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9793542 segs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                           US-10-721-793-115
192
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	u.	115, App	113, App		117, App	151, App	149, App	195, App	193, App		_		_		89, Appl			101, App	105,	103,		147, App	175, App
	Description	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence						
SOMETES	ID	US-10-721-793-115	US-10-721-793-113	US-10-721-793-119	US-10-721-793-117	US-10-721-793-151	US-10-721-793-149	US-10-721-793-195	US-10-721-793-193	US-10-721-793-47	US-10-721-793-45	US-10-721-793-43	US-10-721-793-41	US-10-721-793-91	US-10-721-793-89	US-10-721-793-111	US-10-721-793-109	US-10-721-793-101	US-10-721-793-105	US-10-721-793-103	US-10-721-793-107	US-10-721-793-147	US-10-721-793-175
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df	Query Match Length DB	100.0	100.0	99.2	99.2	81.7	81.7	80.8	80.8	79.2	79.2	78.3	78.3	75.7	75.7	0.99	0.99	64.9	64.9	64.2	64.2	64.1	64.1
	Score	192	192	190.4	190.4	156.8	156.8	155.2	155.2	152	152	150.4	150.4	145.4	145.4	126.8	126.8	124.6	124.6	123.2	123.2	123	123
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Sequence 173, App Sequence 67, Appl Sequence 71, Appl	Sequence 159, App Sequence 163, App Sequence 65, Appl Sequence 69, Appl Sequence 157, App	Sequence 161, App Sequence 139, App Sequence 155, App Sequence 153, App Sequence 137, App Sequence 83, Appl Sequence 81, Appl	Sequence 97, Appl Sequence 167, Appl Sequence 171, Appl Sequence 165, Appl Sequence 169, Appl Sequence 23, Appl Sequence 143, Appl
323 9 US-10-721-793-173 198 9 US-10-721-793-67 198 9 US-10-721-793-71	. თ თ თ თ	323 9 US-10-721-793-161 198 9 US-10-721-793-139 319 9 US-10-721-793-155 323 9 US-10-721-793-153 323 9 US-10-721-793-137 195 9 US-10-721-793-81 274 9 US-10-721-793-81	<b>თთთთთთ</b>
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## ALIGNMENTS

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Sequence 115, Application US/10721793
; Sequence 115, Application US/10721793
; Publication No. US20050065331A1
; GENERAL INFORMATION:
; APPLICANT: Corona Villegas, Miguel
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Gurrola Briones, Georgina
; APPLICANT: Gurrola Briones, Georgina
; APPLICANT: Possani Postay, Lourival Domingos
; APPLICANT: Recentil Lujan, Baltazar
; APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
; ITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: 2099-1070001
; CURRENT APPLICATION NUMBER: US 60/430,067
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 294
; SOROTHARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTHER: PATE: 192
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OTHER INFORMATION: Product= Sodium-channel modifier toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 192; DB 9;
100.0%; Pred. No. 1.1e-53;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Centruroides elegans
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Matches 192; Conservative
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APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Maguel
APPLICANT: Corona Villegas, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Eriones, Georgina
APPLICANT: Gurcola Eriones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the TITLE OF INVENTION: UNIMBER: US/10/721,793
CURRENT APPLICATION NUMBER: US 60/430,067
PRIOR APPLICATION NUMBER: US 60/430,067
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Maguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Briones, Georgina
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTICATION NUMBER: US/10/721,793
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 117
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COATION: (1)...(192)
US-10-721-793-119

NAME/KEY: CDS
NAME/K
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Pred. No. 3.6e-53;
0; Mismatches 1;
                                                                                                        Sequence 119, Application US/10721793
Publication No. US20050065331A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Centruroides elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.5%;
Matches 191; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Recombinant Immunogens for the Genus Centruroides
FILE REPERENCE: 2099.0070001
CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT PILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 113
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (5)..(265)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cy9 is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
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LOCATION: (65)..()
OTHER INFORMATION: Product= Sodium-channel modifier toxin
                                                                                                                                                                                                                                                        Sequence 113, Application US/10721793
Publication No. US20050065331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Centruroides elegans
181 AATAAAAGATGC 192
                                                                    181 AATAAAAGATGC 192
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OTHER INFORMATION:
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LOCATION: (1)..(4)
OTHER INFORMATION:
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NAME/KEY: 3'UTR
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APPLICANT: Garcia Rodrigues, Miguel
APPLICANT: Garcia Rodrigues, Ma Consuelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Garcia Briones, Georgina
APPLICANT: Becarril Lujan, Baltezar
APPLICANT: Possani Postay, Lourival Domingos
ITILE OF INVENTION: Recombinant Immunogens for the Genus Centruroides
ITILE OF INVENTION: Venom of Scorpions of the Genus Centruroides
ITILE OF INVENTION: Venom of Scorpions of the Genus Centruroides
ITILE OF INVENTION: Venom of Scorpions of the Genus Centruroides
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR PILING DATE: 2002-12-02
NUMBER OF SEO ID NOS: 294
SOFTWARE: Patentin version 3.1
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                                                                       AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing, TITLE: that recognize Na+-channels
JOURNAL: Toxicon
VOLUME: 39
ISSUE: 12
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                  LOCATION: (1)..(192)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 81.7%; Score 156.8; DB 9; Best Local Similarity 88.5%; Pred. No. 6.1e-42; Matches 170; Conservative 0; Mismatches 22;
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; Sequence 149, Application US/10721793
; Publication No. US20050065331A1
; Publication No. WESONSONS GENERAL INFORMATION:
; APPLICANT: Corona Villegas, Miguel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Centruroides sculpturatus
                                                                                                                                                                                                                                                 PAGES: 1893-1898
DATE: 2001-12-01
DATES ENTRY DATE:
RELEVANT RESIDUES: (1)..(192)
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181 AATAAAACATGC 192
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NAME/KEY: mat peptide
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NAME/KEY: sig_peptide
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NAME/KEY: CDS
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                                                                                                                    LOCATION: (5)...(265)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
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APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Bossani Postay, Lourival Domingos
APPLICANT: Bossani Postay, Lourival Domingos
APPLICANTON: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
FILE REFERENCE: 2099:0070001
CURRENT FILING DATE: 2003-11-26
FRIOR FILING DATE: 2003-12-02
FRIOR FILING DATE: 2002-12-02
FRIOR FILING DATE: Patentin version 3.1
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ORGANISM: Centruroides sculpturatus
PEATURE:
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                                                     ORGANISM: Centruroides elegans
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Best Local Similarity 99.5
Matches 191; Conservative
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                                                                                                                                                                                                                                                                                   LOCATION: (269)..(
OTHER INFORMATION:
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NAME/KEY: 3'UTR
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NAME/KEY: 5'UTR
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US-10-721-793-151
                                                                                  FEATURE:
NAME/KEY: CDS
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LENGTH: 192
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NAME/KEY: CDS
LOCATION: (5)..(262)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
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; Publication No. US20050065331A1
; GENREAL INFORMATION:
    APPLICANT: Corona Villegas, Miguel
; APPLICANT: Corona Villegas, Miguel
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Garcia Briones, Georgina
; APPLICANT: Garcia Briones, Georgina
; APPLICANT: Becerril Lujan, Baltazar
; APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: US00001
; CURRENT APPLICATION NUMBER: US/10/721,793
; CURRENT ELING DATE: 2003-11-26
; REIOR APPLICATION NUMBER: US 60/430,067
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 193
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
VOLUME: 39
VOLUME: 39
PAGES: 1893-1898
DATE: 2001-12-01
PAGES: LESURE: 1893-1898
DATE: 2001-12-01
RELEVANT RESIDUES: (1)..(192)
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Pred. No. 2.1e-41;
0; Mismatches 23; Indels
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Best Local Similarity 88.0
Matches 169; Conservative
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OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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Sequence 195, Application US/10721793

Publication No. US20050055313A1

GENERAL INFORMATION:

SEQUENCE CONTROL OF THE STATE OF THE STAT
                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D. TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing, TITLE: that recognize Na+-channels JOURNAL: Toxicon VOLUME: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 120
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NAME/KEY: CDS
LOCATION: (1)..(192)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (5)..(262)
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                                                                                                                                                                                                                                                                       LOCATION: (1)..(4)
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                        FEATURE:
NAME/KEY: 3'UTR
LOCATION: (266)..(320)
OTHER INFORMATION:
          LOCATION: (5)..(61) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE: 12
PAGES: 1893-1898
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NAME/KEY: 5'UTR
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US-10-721-793-195
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Sequence 45, Application US/10721793

Sequence 45, Application WS/10721793

Publication No. US20050065331A1

GENERAL INFORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Boseani Postay, Lourival Domingos
APPLICANT: Poseani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Genus Centruroides
TITLE REFERENCE: 2099-007001
CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT APPLICATION NUMBER: US 60/430,067
PRIOR PLING DATE: 2002-11-26
PRIOR PLING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PERCENT APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-12-02
NUMBER: US 60/430,067
SEQ ID NO 45
LENGTH: 258

LENGTH: 258
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OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gl
OTHER INFORMATION: and the last 2 basic aminoacids are cut
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                                       1 AAGGACGGTTATCTGGTCGCAGGCTGCAAAAAGTCTTGCTATAAATTGGGAGAA
                                                                                   61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
      1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA
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Pred. No. 2.8e-40;
0; Mismatches 25; Indel8
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Best Local Similarity 87.0%;
Matches 167; Conservative
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; OTHER INFORMATION:
US-10-721-793-45
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OTHEN INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
AUTHORS: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
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Pred. No. 2.5e-40;
0; Mismatches 25; Indels
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; OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-47
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
LOCATION: (62)..()
OTHER INFORMATION: Product= Sodium-channel modifier toxin
                                                                                                                                                                                                                                                                                                                                                                         Score 155.2; DB 9;
Pred. No. 2.6e-41;
0; Mismatches 23;
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Best Local Similarity 87.0%;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.0%;
Matches 169; Conservative
                                                                                                                                                                                                                                                       ; PAGES: 1893-1898
; DATES: 2001-12-01
; DATABASE ENTRY DATE:
; RELEVANT RESIDUES: (5)..(262)
US-10-721-793-193
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                                                          NAME/KEY: sig_peptide
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LENGTH: 192
                                                                                                                                                                                                                    VOLUME: 39
ISSUE: 12
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PEATURE:
NAME/KEY: CDS
LOCATION: (1)..(204)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
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APPLICANT: Garcia Redriguez, Ma Consuelo
APPLICANT: Garcia Redriguez, Ma Consuelo
APPLICANT: Garcia Briones, Georgiaa
APPLICANT: Garcia Briones, Georgiaa
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Bossani Postay, Lourival Domingos
TITLE OF INVENTION: Venom of Scorpions for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION VUNBER: US/10/721,793
CURRENT APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 294
SOFTWARE PARENTIN VERSION 3.1
SEQ ID NO 91
IENGTH: 198
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; OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 91, Application US/10721793
Publication No. US20050065331A1
GENERAL INFORMATION:
SEQ ID NO 41
LENGTH: 254
TYPE: DA
ORGANISM: Centruroides exilicauda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Centruroides noxius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarıty 66.5
Matches 166; Conservative
                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (205)...(254)
; OTHER INFORMATION:
US-10-721-793-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                         Sequence 43, Application US/10721793

| Sequence 43, Application US/10721793
| Publication No. US20050065331A1
| Garda No. US20050065331A1
| Garda Norman Villegas, Miguel
| APPLICANT: Garcia Rodriguez, Ma Consuelo
| APPLICANT: Becerril Lujan, Baltazar
| APPLICANT: Becerril Lujan, Baltazar
| APPLICANT: Possani Postay, Lourival Domingos
| TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
| TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
| TILE REFERENCE: 2009-0070001
| CURRENT APPLICATION NUMBER: US/10/721,793
| CURRENT PILING DATE: 2003-11-26
| PRIOR APPLICANION NUMBER: US 60/430,067
| PRIOR FILING DATE: 202-12-02
| NUMBER OF SEQ ID NOS: 294
| SEQ ID NO 43
| LENGTH: 192
| LENGTH: 192
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Sequence 41, Application US/10721793

Sequence 41, Application US/10721793

Sequence 41, Application WS/10721793

Sequence 41, Application No. US2005005331A1

GENERAL INFORMATION:

APPLICANT: Corona Villegas, Miguel

APPLICANT: Garcia Roditiguez, Ma Consuelo

APPLICANT: Gurrola Briones, Georgina

APPLICANT: Gurrola Briones, Georgina

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Becerril Lujan, Baltazar

TITLE OF INVENTION: Venom of Scorpions for the Generation of Antivenoms to the

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION: US/10/701/103

CURRENT APPLICATION NUMBER: US/10/721,793

CURRENT PILING DATE: 2003-11-26

PRIOR FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 294

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i LOCATION: (1)..(192)
i OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Centruroides exilicauda
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Sequence 111, Application US/10721793

Sequence 111, Application US/10721793

Publication No. US20050065331A1

GENERAL INFORMATION:

APPLICANT: Corona Villegas, Miguel

APPLICANT: Corona Villegas, Machina

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Valdez Cruz, Norma Adriana

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Possani Postay, Lourival Domingos

TITLE OF INVENTION: Recombinant Immunogens for the Genus Centruroides

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION NUMBER: US/10/721,793

CURRENT FILING DATE: 2003-11-26

PRIOR PILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 294

SOFTWARE: PatentIn version 3.1

TENGRE DATE: DATE: 2003-11-26

SEQ ID NO 111

TENGRE DATE: 2003-11-20
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                                                                                                                                 182 recracedarinesenscranisteaaganistecearagracacedacrisececer 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AAGGACGGTTATCTGGTGAACAAGACGGGCTGCAAATACAATTGCTGGATATTGGGAGAA 63
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66.0%; Score 126.8; DB 9; Length:
Best Local Similarity 82.8%; Pred. No. 6.4e-32;
Matches 159; Conservative 0; Mismatches 27; Indels
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; OTHER INFORMATION: Product= Sodium-channel modifier toxin US-10-721-793-111
                                                                           118 TGCTACGGATTTGGGTGCTATTGCGAAGGATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search.completed: January 22, 2006, 01:12:50 Job time : 2178 secs
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ORGANISM: Centruroides elegans
                                                                                                                                                                                                               178 TCTAATAAAGATGC 192
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NAME/KEY: CDS
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Sequence 89. Application US/10721793

Publication No. US20050055331A1

GENERAL INFORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Gurical Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Vecombinant Immunogens for the Genus Centruroides
TITLE OF INVENTION: Vecombinant Immunogens for the Genus Centruroides
TITLE OF INVENTION: Vecombinant Immunogens for the Genus Centruroides
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TITLE OF INVENTION: Vecombinant Immunogens for the Genus Centruroides
TITLE OF INVENTION: Vecombinant Immunogens for the Genus Centruroides
TITLE OF INVENTION IMMUNOGENTION 
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                                                                                                                                                                                                                                                          GAAAACGAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTAT 117
                                                                                                                                               61 gaaaacaaaaacrigcgararggaargcaaagcgaaggaaccaaggaggragrracggcrar 120
                                                                                                                                                                                                                       118 TGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTT 177
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              1 AAGGAAGGTTATCTGGTGAACAAAAGCACAGGCTGTAAATACAACTGCTTGATATTGGGA 60
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LOCATION: (62)..()
OTHER INFORMATION: Product= Sodium-channel modifier toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 145.4; DB 9;
Pred. No. 4.9e-38;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.7%;
Best Local Similarity 87.7%;
Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             181 CCTAATAAAACATGC 195
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NAME/KEY: sig_peptide
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NAME/KEY: 3'UTR
LOCATION: (269)..(3
OTHER INFORMATION:
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; OTHER INFORMATION
US-10-721-793-89
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LOCATION: (5).
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AU119061 AU119061
DN839051 SMC-1_05
CF503342 MF1-0018U
BU55252 AGENCOURT
CR899083 SUB SECOTÉ
BQ664839 QCGZ7N10.
BU543170 AGENCOURT
AY440472 Armiggeres
DR423779 nav30d12.
NF578 zata265.81
NF578 242605.81
AG725129 HS 5392 A
CL644174 CH215-52P
CL644174 CH216-52P
CL644174 CH216-52P
CL64417 Pan trogl
AA233053 zt54605.r
BF767499 CM4-CN009
                                                                            January 21, 2006, 21:29:01; Search time 8943 Seconds (without alignments) 1004.486 Million cell updates/sec
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                                                                                                                                                             1 aaagacggttatctggtgga......ccctttctaataaaagatgc 192
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                41078325 seqs, 23393541228 residues
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Maximum Match 100%
Listing first 45 summaries
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CNS00JOB
AUI)9061
DN839051
GP503342
BU55252
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AQ725129
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                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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192
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Match Length DB
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CC453499 ZWMBBC033 CC647597 NDL.128M1 BX970645 Reverse 8 BX456789 BX33631 BX332631 BX332631 BX332631 BX332631 BBC31242 601676224 BBC91242 601676224 BBC91242 601676224 BBC91242 601676224 BBC91246 601676224 BBC91246 601676224 BBC722903 H03 Foste CB285819 CMD25_C01 AJ6959518 AJ657416 DN107120 1104538 M AJ995538 AJ939538 CF176758 855141 MA CE7787263 855141 MA CB787263 855141 MA	ALIGNMENTS  582 bp mRNA linear EST 15-SEP-2004 .library, embryo kidney Homo sapiens cDNA clone nce.  323  Chordata; Craniata; Vertebrata; Buteleostomi; Buarchontoglires; Primates; Catarrhini; .,R., Shirota,M., Sakakibara,Y., Chiba,J., Nakai,K. and Sugano,S. of human and mouse genes reveals a homologous he promoter regions 1711-1718 (2004) ki Minatoku, Tokyo 108-8639, Japan hilfiers Homo sapiens" "RNA" "RNA" "RNA" "RNA" "RNA"	y" cDNA library, embryo kidney"
9 CC453499 9 CC847597 10 BX970645 5 BX436789 5 BX436789 2 BX32631 5 BX32631 5 BX32631 5 BX32631 6 CR228903 6 CR22903 6 CR22903 6 CR22903 6 CR722903 6 CR725903 6 CR725903 6 CR7258 6 CR7258 6 CR7363 6 CR77678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 7 Ay93953 8 BX974 6 CR77678 6 CR77678 6 CR77678 6 CR77678 7 Ay93953 8 BX974 6 CR77678 6 CR77678 6 CR77678 6 CR77678 7 Ay93953 8 BX974 6 CR77678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 7 Ay93953 8 BX97678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 7 Ay93953 8 BX97678 6 CR77678 6 CR77678 6 CR77678 6 CR77678 7 Ay93953 8 BX97678 6 CR77678 6 CR77678 7 CR77678 7 CR77678 7 CR77678 7 CR77678 7 CR77678 7 CR77678		ğ Öo
17.2 7619 17.2 7619 17.2 933 17.2 1013 17.1 1013 17.1 246 17.1 17.1 17.1 17.1 17.1 17.1 17.1 17.1	BP248044 BP248044, mRNA sequence. BP248044, mRNA sequence. BP248041. GI:52130323 BSG. BSG. HOMO sapiens (human) HOMO sapiens MAMMANIA (P. 7. Yamashita, R. / Mizushima-Sugano, J. , Naka Sequence comparison of halock structure in the proposer of t	/tissue / /cell_lTn /dev_stag /clone_l1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BP246044 LOCUS DEFINITION BP246 ACCESSION BP246 KEYWORDS SST. CORGANISM HOMO ORGANISM HOMO ORGANISM HOMO TITLE SEQUE TOWNED GEOOF TOWNED GEOOF TOWNED GEOOF TOWNED GEOOF TOWNENT GEOOF TOWNENT DEPARA DEPARTURES SOURCE	ORIGIN

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Gaps ö

DB 3; Length 582;

Query Match
19.2%; Score 36.8; DB 3; Length 50
Best Local Similarity 50.0%; Pred. No. 2;
Matches 92; Conservative 0; Mismatches 92; Indels

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We waw genoscope.cns.fr)

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers
                                                                                                                                  CNS00JOB 982 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR38N08 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU119061 B20 bp mRNA linear EST 01-AUG-2002 AU119061 HEMBA1 Homo sapiens cDNA clone HEMBA1004961 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 CGAGGAGGTAATTACGGCTATTGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGAT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   654 ARCGSGGAAAAAAYGRCWGWWSTCWTGCTTTTCTYKTTYMGTVYMAAAAAAWWAAAMAWW 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 TACACTTGCTGGATATTGGGAGAAAACAAATACTGCAATAGGGAATGCACATGGAAGCAC
                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTVAMAMAMMITTSAVACATWWAMAAAAMACA 562
584 AATGAATCCTGTCCAAATTGCTCGTGGGATTG 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.2%; Score 35, DB 1
ilarity 32.0%; Pred. No. 8.1;
Conservative 42; Mismatches
                                                                                                                                                                                                                       £1y), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BACR38N08"
/clone_lib="RPCI-98"
/note="end : TET3"
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AU119061.1 GI:10934296
EST.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope
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                                                                               RESULT 3
CNS00JOE/c
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                           DEFINITION
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AUTHORS
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/dev_stage="mature"
/clone lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                                                                                                                            BF640569 EST 19-DEC-2000 NF031A09IN1F1068 Insect herbivory Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                        121 TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT 180
                                                                                                                                                   271 CTGGGAAAACCATTTAAAACGAAATGATTCTATCATAGTAGATATTTCATGCCTTTT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Pabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 GGTTAAATTGGTGAGACAAGCTGGTGCAAAAACCAATATCTTAGTTGGTGATGGCTCAAC 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 TACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGCTACGGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GGTTATCTGGGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGGAGAAACAAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 656)
Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
AACAAATACTGCAATAGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
                                                   211 ACCATATATACAATTAAAAGATGCAGATGGAAGGCCAGATAAGGTGGTTGCCGAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue type="local and systemic leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .656
/organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kkorth@comp.uark.edu
Insert Length: 656 Std Error: 0.00
Plate: 011 row: A column: 09
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF031A091N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF031A09IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Score 34.8; DB
Pred. No. 9.1;
0; Mismatches
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Lafayette, IN 47907-1153, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 18.1%;
1 Similarity 57.3%;
63; Conservative (
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                    Tel: 765 494 0494
Fax: 765 496 7213
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Weng,J.-K., Tanurdaic,M. and Chapple,C.
Functional analysis and comparative genomics of expressed sequence
tags from the lycophyte Selaginella moellendorffii
BMC Genomics 6 (1), 85 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 TTGCTGGATATTGGGAGAAAACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGG 101
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Lycopodiophyta, Isoetopsida, Selaginellales, Selaginellaceae;
                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                        Tel: 81-438-52-3975
Fax: 81-438-52-3966
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNB39051 Selaginella moellendorffii cDNA library SmoC-1 Selaginella moellendorffii cDNA library SmoC-1 Selaginella moellendorffii cDNA 5, mRNA sequence.
                                                                                       Hominidae; Homo.
1 (bases 1 to 820)
Ota T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Ota T., Nishikawa,T., Suzuki,A., Nakamura,Y., Nagai,T., Sugano,S. and
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609 ińcciegagangaegancacacaganganganganaragemengiegaegagagagaga
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="texon:9606"

/clone="HEMBA1004961"

/tissue type="whole embryo, mainly head"

/clone lib="HEMBA1"

/note="Vector: pMB188FL3"
                                                                                                                                                                                                                                                                    Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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Selaginella moellendorffii
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Department of Biochemistry
Purdue University
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                                                                                                                                                                                       human cDNA project
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Contact: Takao Isogai
Genomics Laboratory
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            sapiens (human)
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Bukaryotta; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosoma.

1 (Bases 1 to 340)

Demarco, Kowaltowski, A.T., Machado, A.A., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, M.C., Dias-Neto, E., Leite, L.C.C. and Verjovski-Almeida, S. and Perere, four novel retrotransposons with high transcriptional activities from the human parasite Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 30-APR-2004
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Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Faxi +55-11-3091-2081
Faxi +55-11-3091
Faxi +55-1
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Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GITATICTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAAAAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pDNR-LIB; Site 1: Sfil; Library construction was performed according to manufacture's (CLONTECH, Palo Alto, CA) recommended protocol for Creator Smart cDNA Library Construction
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|clone lib="Selaginella moellendorffii cDNA library
| cmc-ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AGTCTCTTTGAAAATGCCCCGGAACTTAATGAGGTGGAAATTACGGCTAT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 ACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTAT 117
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/organism="Selaginella moellendorffii"
/mol_type="mRNA"
/db_xref="taxon:88036"
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Emall: C. PCR PRimers
FORP PRIMERS
FORWARD: M13 Backward
BACKWARD: M13 Backward
Plate: SmoC-1 05 row: A column: 23
Seq primer: T'Forward
Location/Qualifiers
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/note="Organ: Crown and leaf; Vector: pCMV.SPORTG, Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 2006 from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20c, wheat plants were transferred to 4C in growth at 20C, wheat plants were transferred to 4C in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inticum aestivum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticae; Triticum.

I (bases 1 to 1080)

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,

Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,

Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,

Penniket,C., Roach,J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Unpublished (2003)

Contact: Patrick Gulick

Plant Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR738811 18-JUL-2005 FGAS084028 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum aestivum CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: pgulick@alcor.concordia.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [105,489].
Plate: LGB202 row: N column: 17.
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/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6_CAP GATE 1"
                                                                                                                                                                                                                                                                                                                                                                                            102 AGGIAATTACGCCTATTGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTAC
                                                                                                                                                                                                                                                  42 TTGCTGGATATTGGGAGAAAAAAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGG
                                                                                                                                                                                                                                                                                                                     644 TTGCTGGAGATGAGGATCACACAGATGGAGTAGTAGCTTGTGCTGCTGGACTAATAGGGG
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                                                                                                    Length 918;
                                                                                                                                                                               Indels
Note: this is a NIH_MGC Library."
                                                                                                            DB 5;

    .1080
    /organism="Triticum aestivum"

                                                                                                    18.0%; Score 34.6; Di
55.4%; Pred. No. 11;
cive 0; Mismatches
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Matches 67; Conserv
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: porB7; Site_1: XhoI;
/note="Organ: prostate; Vector: porB7; Vector: prostate; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BUS52525 918 bp mRNA linear EST 16-SEP-2002 AGENCOURT_10333015 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6576318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 GTAACTCCACTTTCTGGATAAAATCTGAATTCAGCTATTGAATTAGCAATAGAATCCGGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 AGCACCGAGGAGGTAATTACGGCTATTGCTACGGATTTGGGTGCTATTGCGAAGGATTGT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.

I (bases 1 to 918)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 GCAAATACACTTGCTGGATATTGGGAGAAAACAAATACTGCAATAGGGAATGCACATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 GTCATAGAGGAATTAGACACATCAGTTCTTGAGGATATCGACATATTTTTGACTAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.6; DB 6; Length 340; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="Mesocricetus auratus"
/clone_lib="MRI-0018"
/note="Yector: Sureclone"
                             'organism="Schistosoma mansoni"
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/db_xref="taxon:6183"
/clone="MF1-0018U-V031-H07.B"
                                                                                                                                                                                                                                                                                                                                                                                                    18.0%; Scc. No. 0.54.3%; Pred. No. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6576318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 736.
Location/Qualifiers
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                                                                                                                                                                        sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 CCGATAGTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 TCGATAGGA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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BU552525
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Gaps ö 61

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/db.xxon:4236"
/db.xxon:4236"
/clone="QGC27N10"
/lab host="B.coli"
/clone|lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRCDNASfiAB; The library was constructed
/note="Vector: pBRCDNASfiAB; The library was constructed
/note=properated unique 5' and 3' tags to distinguish each
source of RNA. cnNAB were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_SEQ=Not found"
                                                                                                                                                                                                                                                                                                  Agoowasy 490 bp mRNA linear EST 14-AUG-2002 QGC27N10.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QGC27N10, mRNA sequence.
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                                                                                            455 AAGGTGGGTAACTGATGAACAACTCTGACTGCAGACTCACTTCTTATTCTGGGAGAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactuca sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorloideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
University of California at Davis (UCD)
Davis, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Delongs to config.
Delongs to contig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cichorieae; Lactuca.

1 (bases 1 to 490)
Kozika. Michelmore.R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaudh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAAAAA
                                               2 AAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
17.8%; Score 34.2; DB 5; Length 490;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 72; Conservative 0; Mismatches 63; Indels
33; Indels
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lactuca sativa"
                                                                                                                                                                                                   395 gradacaracrargereracecarar 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C27 row: N column: 10.
                                                                                                                                                   62 ACAAATACTGCAATAGGGAATGCACAT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ864839.1 GI:22250314
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  54; Conservative
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the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCACGAGGACTGAACTGAACGAGTAAGAAA)."
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Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 GGGGGCGTGTCCCATCTGCAGGGGCTTGTTGTTGTGAGGAGGCAGAGACTGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral elements Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
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Rogel-Gaillard, C., Bourgeaux, N., Billault, A., Vaiman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 459)
Chardon, P., Iamuccelli, N., Roig, A., Dossat, C., Demars, J.,
Rogel-Gaillard, C., Roy, A., Schibler, L. and Milan, D.
A physical map of the swine genome
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/clone_lib="SBAB"
/note="Genoscope sequence ID : IHOAAA26AA06FM1"
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Best Local Similarity 60.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 36; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; Bac-end sequence BES; Genome Survey Sequence.
Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa BES, genomic survey sequence.
CR899083
CR899083.1 GI:56223580
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/strain="Large White"
/db_xref="taxon:9823"
/clone="b10260D02"
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e_lib="SBAB"
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Location/Qualifiers
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Mammalia; Eutheria;
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3 (bases 1 to 459)
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Best Local Similarity
Matches 67; Conserv
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                   LOCUS
DEFINITION
ACCESSION
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ORGANISM
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   4X440472/c
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AUTHORS
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AUTHORS
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JOURNAL
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DR423779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="taxcan:9606"
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/clone lib="NIH MGC 40"
/clone lib="NIH MGC 40"
/clone lib="NIH MGC 40"
/clone lib="NIH MGC Library constructed by litectionally cloned into EcoR1/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                            BUS43170 893 bp mRNA linear EST 13-SEP-2002
AGENCOURT_10338811 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6575177
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648 TIGCIGGAGAIGAGGAICACACAGAIGGAGIAGCIIGIGCIGCIGGACIAAIAGGGG 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           708 ACTTATCTACACCATTTCNGAAGGATCNTACTGAATTACTAGAGCTAGGCCAATGATCC 767
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

I (basea I to 893)

NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 TTGCTGGATATTGGGAGAAAACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://imago.llnl.gov
Plate: LLCM2771 row: k column: 17
High quality sequence stop: 578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                      BU543170.1 GI:22853653
                                                         CGGATTTGGGTGCTA 137
                                                                                 157 CGGGTTTGGGTCCAA 171
                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                              5', mRNA sequence.
BUS43170
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Best Local Similarity
Matches 66; Conserv
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TITLE
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BUS43170
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RESULT 12

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Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Ruchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Mappl, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M. Direct Submission
                                                                                                                                                                                                                                           Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera; Culicoidea,
Culicidae, Culicinae, Culicini, Armigeres, Armigeres.

1 (bases 1 to 748)

Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Tiss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
Fuchs, J.F., Taso, I.-Y., Hang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
Christensen, B.M.

Description of the Transcriptomes of Immune Response-Activated
Hemosytes from the Mosquito Vectors Aedes aegypti and Armigeres
HTC 20-0CT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 rgargaagraangcogcrrrrigrogcreargreegrecreccocococrerrearccogr 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at https://asap.ahabs.wisc.edu/annotation/php/logon.php.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Armigeres subalbatus"
/mol_type="mRNA"
/isolation source="perfused hemolymph of bacteria-innoculated organisms at 1, 3, 6, 12, and 24 hours post-innoculation"
/db_xref='taxon:124917"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-OCT-2003) Animal Health and Biomedical Sciences University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               More information about this sequence is available in ASAP (A
   AY440472 1inear HTC 2
Armigeres subalbatus ASAP ID: 39205 unknown mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immun. 72 (7), 4114-4126 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="hemocyte"
/tissue_type="hemolymph"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="ASAP:39205"
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                                                                                                              AY440472.1 GI:42765501
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                                                                                                                                                                                Armigeres subalbatus
                                                                                                                                                                                                                         Armigeres subalbatus
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

ACCESSION

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yv56e03.s1 Soares fetal liver spleen lNPLS Homo sapiens cDNA clone IMAGE:246748 3' similar to gb:X58957 TYROSINE-PROTEIN KINASE ATK (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
Unpublished (1995)
Contract: Wilson RK
Washington University School of Medicine
4444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AGACAGACTGAATTTTGCGATGAAATATTTTTTAGGAGGAGGATGTAAATAGCCGCACA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 GAGGAGGTAATTACGGCTATTGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATA 157
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                         To (bases 1 to 377)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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Best Local Similarity 52.9%; Pred. No. 18;
Matches 72; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens".
/mol_type="mRNA"
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/db_xrefe="taxon:9606"
/clone="IMAGE:295208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GTACACCGACTTGGCC 173
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N75948.1 GI:1238526
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                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                        VERSION
KEYWORDS
SOURCE
                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pterygium"
/tissue_type="Pterygium"
/lab_host="EMDH10B"
/lab_host="EMDH10B"
/clone_lib="Human pterygium. Unnormalized (nav)"
/note="Organ: Bye; Vector: pCWVSporte; RNA was extracted
from 9 pooled human pterygia. A directionally cloned cDNA
library in the pCMVSPORTe vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)
Passentially following the protocols of the SuperScript
Plasmid System, full details of which are contained in the
manufacturer's Instruction manual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carried out using a Not I primer-adapter [5.-pgAcTAGTTCTAGATCGCGGCGCCCC(T)15-3']. CDNA was [5.-pGACTAGTTCTAGATCGCGAGCGCCCC(T)15-3']. CDNA was choed in Not I/sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC). Analyzed data available through http://neibank.nei.nih.gov."
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704 bp mRNA linear BST 29-JUN-2005
nav33012.y1 Human pterygium. Unnormalized (nav) Homo sapiens CDNA
Clone nav30d12 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 TGGATATTGGGAGAAAACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 racharradgahahaccararraranararrahahagargcagaragaragaranggr 248
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                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 704)
Wistow, G., Jaworski, C., Aryankalayil-John, M., Rowsey, J.J., Cox, C.,
Wistow, G., Jaworski, C., Aryankalayil-John, M., Rowsey, J.J., Cox, C.,
Reid, T., Dushku, N. and Carper, D.
NEIBank analysis of Human pterygium
Unpublished (2005)
Contact: Wistow G
                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
et : 301 402 3452
Fax: 301 496 0078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: graeme@helix.nih.gov
Plate: 30 row: d column: 12
Seg primer: Universal M13 Reverse.
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I (bases 1 to 474)

Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Gish, W.,
Chissoe, S., Dietrich, N., DuBuque, T., Lacy, M., Le, M., Le, N.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Hawkins, M., Hultman, M., Roans, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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                                         Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: esr@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 372 Std Brror: 0.00
Seq primer: and 3-40 forward
High quality sequence stop: 342.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 33.6; DB 8; Length 474; 52.9%; Pred. No. 19; tive 0; Mismatches 64; Indels 0
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Job time : 8948 secs
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clone="IMAGE:246748"
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                     sapiens (human)
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Best Local Similarity 72. Conservative
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KEYWORDS
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
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150.4

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invention describes immunogenic or antigenic compositions comprising a scorpton toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the invivo effects of scorpton venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centruroides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stungs. This polymucleotide is a DNA sequence encoding the mature protein of a sodium channel modifier toxin isolated from a scorpion of the Centruroides genus, given in an exemplification of the
The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
888888888888888888888
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Sequence 192 BP; 59 A; 35 C; 53 G; 45 T; 0 U; 0 Other;

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180
                                                                                                                                                                                                                      121 TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCCGACTTGGCCCCTTTCT 180
                                                                                                     9
                                                                                                                                                         AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
                                                                     1 AAAGACGCTTATCTGGTGGACAAGACGGCTGCAAATACACTTGCTGGATATTGGGAGAA
                                                                                              AAAGACGGTTATCTGGTGGACAAGACGGCTGCAAATACACTTGCTGGATATTGGGAAA
                                                                                                                                      AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
                                                                                                                                                                                                    TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT
                                         Gaps
                                         ö
        DB 14; Length 192;
                                       Indels
Score 192; DB 14;
Pred. No. 5e-55;
        100.0%; Sci
100.0%; Pri
tive 0; 1
                                                                                                                                                                                                                                                                  181 AATAAAAGATGC 192
                                                                                                                                                                                                                                                                                                AATAAAAGATGC 192
                                       Matches 192; Conservative
      Query Match
Best Local Similarity
                                                                                                                                      61
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DNA encoding the full length scorpion Cel3 toxin protein Seg 113. ADY85769 standard; DNA; 323 BP. (first entry) 02-JUN-2005 ADY85769; 

gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis.

Centruroides elegans,

US2005065331-A1.

24-MAR-2005.

26-NOV-2003; 2003US-00721793.

UNIV MEXICO NACIONAL AUTONOMA. LAB SILANES SA DE CV. 02-DEC-2002; 2002US-0430067P. (UYME-) UNIV

(SILA-)

Becerril LB; Valdez CNA, Gurrola BG, Garcia RMC, Corona VM, (Possani PLD;

WPI; 2005-252753/26. P-PSDB; ADY85770. Novel isolated scorpion toxin polypeptide, useful for preventing

(UYME-) UNIV MEXICO NACIONAL AUTONOMA.

02-DEC-2002; 2002US-0430067P.

This invention relates to novel scorpion toxin polynuclectides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Bug type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centruroides. Furthermore, it provides a diagnostic method that uses an immunoglobalina present in a sample that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In great an addition, it provides methods that are useful for treating envenomention from scorpion stings. This polynucleotide is a DNA sequence encoding the from scorpion of the Centruroides genus, given in an exemplification of the 184 envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides. 124 120 180 244 9 125 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 185 TACGGATITGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT 1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA 65 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA 61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGGAGGAGGTAATTACGGCTATTGC Gaps ; 0 Length 323; DNA encoding the scorpion Cel3b toxin mature protein Seq 119. Indels gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis. Sequence 323 BP; 99 A; 56 C; 82 G; 86 T; 0 U; 0 Other; Query Match
100.0%; Score 192; DB 14;
Best Local Similarity 100.0%; Pred. No. 6.1e-55;
Matches 192; Conservative 0; Mismatches 0; Claim 1; SEQ ID NO 113; 135pp; English. BP. 26-NOV-2003; 2003US-00721793 ADY85775 standard; DNA; 192 (first entry) AATAAAAGATGC 192 245 AATAAAAGATGC US2005065331-A1 02-JUN-2005 24-MAR-2005. invention. 121 ADY85775; 181 RESULT 3 ADY85775 셤 요 셤 g ଚ ઠે ð ₹

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This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the caperation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the gamus centruroides. Purthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stings. This polynucleotide is a DNA sequence encoding the mature protein of a sodium channel modifier toxin isolated from a corpion of the Centruroides genus, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 120
                                                                                                                                                       Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAGACGGITAITCIGGTGGACAAGACGGGCTGCAAAIACACTIGCIGGATAITGGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding the full length scorpion Cel3b toxin protein Seq 117.
                                      Gurrola BG, Valdez CNA, Becerril LB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 190.4; DB 14; Length 192; Pred. No. 1.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ds; toxin; sodium channel; immunogenicity; antigen;
antibody production; venom; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 192 BP; 59 A; 36 C; 53 G; 44 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 119; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADY85773 standard; DNA; 323 BP.
(SILA-) LAB SILANES SA DE CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.5%;
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2005 (first entry)
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                                           Garcia RMC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centruroides elegans
                                                                                                       2005-252753/26.
                                                                                                                        P-PSDB; ADY85776.
                                        Corona VM, Possani PLD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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This invention relates to novel scorpion toxin polymucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention toxin protein or Iragment thereof, which and neutralize the in scorpion toxin protein or Iragment thereof, which and neutralize the in cyivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centuroides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the species of scorpion that has tung an individual through the detection of identifying antibodies. In from a cadition, it provides methods that are useful for treating envenomation from scorpion stings. This polynucle is a DNA sequence encoding the first secretion of the Centruroides genus, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AACAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT 180
                                                                                                                                                                                                                                                                                                                     Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA
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                                                                                                                                                                                                     Gurrola BG, Valdez CNA, Becerril LB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 190.4; DB 14; Length 323;
Pred. No. 2.1e-54;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 323 BP; 99 A; 57 C; 83 G; 84 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 117; 135pp; English
                                                                                                                                           (UYME-) UNIV MEXICO NACIONAL AUTONOMA. (SILA-) LAB SILANES SA DE CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.24;
                                                                       26-NOV-2003; 2003US-00721793
                                                                                                           02-DEC-2002; 2002US-0430067P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.5
Matches 191; Conservative
                                                                                                                                                                                                           Garcia RMC,
                                                                                                                                                                                                                                                                   WPI; 2005-252753/26.
P-PSDB; ADY85774.
US2005065331-A1.
                                                                                                                                                                                                             Corona VM, (
Possani PLD;
                                     24-MAR-2005
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ID ADY8
XX
AC ADY8
XX
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 В
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Gaps

120 180 180

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Gaps

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Indels

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BP.

ADY85807 standard; DNA; 192

ADY85807;

DNA encoding the full length bark scorpion CsEvIa toxin protein Seq 149.

ADY85805 standard; DNA; 320 BP.

181 AATAAAACATGC 192

02-JUN-2005 (first entry)

ADY85805;

gene; ds; toxin; sodium channel; immunogenicity; antigen;

antibody production; venom; vaccine; diagnosis

Centruroides sculpturatus

US2005065331-A1

24-MAR-2005.

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ADY8580
                                                            RESULT
                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel scorpion toxin polymucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can appropriate recombinant fusion proteins in the development of vaccines that can pervent envenomention from stings of scorpions of the genus contraroides. Purthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunogioulum spream that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In a sample that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In a mature protein of a sodium channel modifier toxin isolated from a mature protein of a sodium channel modifier toxin isolated from a invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
                                       DNA encoding the bark scorpion CsEvIa toxin mature protein Seq 151.
                                                                                                                                                                                                                                                                                                                                                                                                            Gurrola BG, Valdez CNA, Becerril LB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 192;
                                                                               gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 192 BP; 62 A; 32 C; 51 G; 47 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 156.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 151; 135pp; English.
                                                                                                                                                                                                                                                                                                                                               (UYME-) UNIV MEXICO NACIONAL AUTONOMA.
(SILA-) LAB SILANES SA DE CV.
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                                                                                                                                                                                                                                                                    26-NOV-2003; 2003US-00721793.
                                                                                                                                                                                                                                                                                                       02-DEC-2002; 2002US-0430067P
(first entry)
                                                                                                                                            Centruroides sculpturatus.
                                                                                                                                                                                                                                                                                                                                                                                                              Garcia RMC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-252753/26.
P-PSDB; ADY85808.
                                                                                                                                                                                    US2005065331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                            Corona VM, Possani PLD;
  02-JUN-2005
                                                                                                                                                                                                                          24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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Becerril LB;

Valdez CNA,

Gurrola BG,

Garcia RMC,

Corona VM, Possani PLD;

WPI; 2005-252753/26. P-PSDB; ADY85806.

(UYME-) UNIV MEXICO NACIONAL AUTONOMA. (SILA-) LAB SILANES SA DE CV.

02-DEC-2002; 2002US-0430067P. 26-NOV-2003; 2003US-00721793.

This invention relates to novel scorpion toxin polymuclectides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centrucides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the specific immunoglobulins present in a sample that can detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation addition, it provides methods that are useful for treating envenomation from scorpion stings. This polymucleotide is a DNA sequence encoding the full length protein of a sodium channel modifier toxin isolated from a scorpion of the Centruroides genus, given in an exemplification of the Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides. 61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 120 62 AAGGACGGTTATCTAGTGGAAAAGACGGGCTGCAAAAAGACTTGCTACAAATTGGGAGAA 121 9 1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA Gaps ; ` DB 14; Length 320; 22; Indels Sequence 320 BP; 100 A; 51 C; 80 G; 89 T; 0 U; 0 Other; 81.7%; Score 156.8; DB 1 88.5%; Pred. No. 5.9e-43; iive 0; Mismatches 22 Claim 1; SEQ ID NO 149; 135pp; English Conservative Query Match Best Local Similarity Matches 170; Conserv Invention

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Gaps

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22; Indels

Pred. No. 4.9e-43; 0; Mismatches 22

Best Local Similarity 88.5 Matches 170; Conservative

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1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA 1 AAGGACGGTTATCTAGTGGAAAAGACGGGCTGCAAAAAGACTTGCTACAAATTGGGAGAA 셤 ð

AATAAAGATGC 192

181

121

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Gaps

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Indels

23;

Score 155.2; DB 1 Pred. No. 1.7e-42; 0; Mismatches 23

Similarity

Query Match

DB 14; Length 192;

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Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
241
                                     TACGGATTTGGGTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT
                                                                                                                                                                           DNA encoding the bark scorpion CsElx toxin mature protein Seq 195.
                                                                                                                                                                                                                                                                                                                                  Gurrola BG, Valdez CNA, Becerril LB;
                                                                                                                                                                                         gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 195; 135pp; English.
                                                                                                                                                                                                                                                                                                          (UYME-) UNIV MEXICO NACIONAL AUTONOMA.
(SILA-) LAB SILANES SA DE CV.
                                                                                                                         ADY85851 standard; DNA; 192 BP
                                                                                                                                                                                                                                                                                           02-DEC-2002; 2002US-0430067P.
                                                                                                                                                                                                                                                                          26-NOV-2003; 2003US-00721793
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                       Centruroides sculpturatus.
                                                             AATAAAAGATGC 192
                                                                              AATAAAACATGC 253
                                                                                                                                                                                                                                                                                                                                     Garcia RMC,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-252753/26.
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Possani PLD;
                                                                                                                                                            02-JUN-2005
                                                                                                                                                                                                                                                         24-MAR-2005
                                                                                                                                           ADY85851;
                            121
                                              182
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This invention relates to novel scorpion toxin polynuclectides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprisions a scorpion toxin protein or fragment thereof, which can be used for the composition toxin protein or fragment thereof, which can be used for the comparation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centuroides. Purthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stings. This polymucleotide is a DNA sequence encoding the mature of the protein of a sodium channel modifier toxin isolated from a mannel. scorpion of the Centruroides genus, given in an exemplification of the invention

Sequence 192 BP; 62 A; 29 C; 54 G; 47 T; 0 U; 0 Other;

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This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Brg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the secret or appropriate recombinant fusion proteins in the development of vaccines or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenmention from strings of scorpions of the genus centruroides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins immunogent in a sample that can determine the species of scorpion that has
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                                                                                                                              AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
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(SILA-) LAB SILANES SA DE CV.
                                                                                                                                                                                                                                                                                                                                                                                     ADY85849 standard; DNA; 320 BP.
80.8%; S
milarity 88.0%; P
Conservative 0;
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                      Best Local Sim
Matches 169;
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stung an individual through the detection of identifying antibodies.
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Pred. No. 2.1e-42;
0; Mismatches 23; Indels
                                                                                                                  Sequence 320 BP; 99 A; 49 C; 85 G; 87 T; 0 U; 0 Other;
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Best Local Similarity 88.0%;
Matches 169; Conservative
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Becerril LB; DNA encoding the bark scorpion Cex10 toxin mature protein Seq gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis. Valdez CNA, (UYME-) UNIV MEXICO NACIONAL AUTONOMA (SILA-) LAB SILANES SA DE CV. Gurrola BG, BP. 26-NOV-2003; 2003US-00721793 02-DEC-2002; 2002US-0430067P. ADY85703 standard; DNA; 192 (first entry) Garcia RMC, Centruroides exilicauda US2005065331-A1. 02-JUN-2005 24-MAR-2005. ADY85703; RESULT 9

47.

Corona VM, Possani PLD;

WPI; 2005-252753/26. P-PSDB; ADY85704, Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.

Claim 3; SEQ ID NO 47; 135pp; English.

This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present

Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation

WPI; 2005-252753/26. P-PSDB; ADY85702.

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           scorpton toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpton venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus immunogenic matrix for the purification of specific immunogenic matrix for the purification of specific immunogeniums stung an individual through the detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stings. This polynucleotide is a DNA sequence encoding the mature protein of a sodium channel modifier toxin isolated from a
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                                                                                                                                                                                                         scorpion of the Centruroides genus, given in an exemplification of the
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 compositions comprising
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Pred. No. 2.1e-41;
0; Mismatches 25; Indels (
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                                                                                                                                                                                                                                                        Sequence 192 BP; 57 A; 34 C; 52 G; 49 T; 0 U; 0 Other;
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 invention describes immunogenic or antigenic
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LAB SILANES SA DE CV.
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                                                                                                                                                                                                                                                                                                     87.0%;
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Matches 167;
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Matches 167; Conservative Centruroides exilicauda US2005065331-A1. 02-JUN-2005 24-MAR-2005 nvention ADY85699; Query Match RESULT 11 유 셤 8 셤 ઠે 셤 ò ò

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This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Brg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centrarise for the purification of specific immunoglobulins present in a sample that can determine the species of scorpion that has corps in individual through the detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stings. This polymucleotide is a DNA sequence encoding the mature protein of a sodium channel modifier toxin isolated from a corpion of the Centruroides genus, given in an exemplification of the
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Pred. No. 7.3e-41;
0; Mismatches 26; Indels
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antibody production; venom; vaccine; diagnosis.
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                           valdez CNA,
                                                                                                                                                                                                                                                                                            envenomation from scorpion stings, and as vacc. from venom of scorpions of genus Centruroides.
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                               Gurrola BG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAAAAGATGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AATAAATCATGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 166; Conservative
                               Garcia RMC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centruroides exilicanda
                                                                                                                                            WPI; 2005-252753/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                   P-PSDB; ADY85700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2005065331-A1
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                                   Corona VM,
Possani PLD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADY85697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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DNA encoding the Mexican scorpion Cn10b toxin mature protein Seq 91.

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This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can aprevent envenomation from stings of scorpions of the genus centruroides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the specific immunoglobulins present in a sample that can determine the specific immunoglobulins grung an individual through the detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation to scorpion stings. This polynucleotide is a DNA sequence encoding the interval accorpion of the Centruroides genus, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                            Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
                                                                                                                                                                                                                                      Garcia RMC, Gurrola BG, Valdez CNA, Becerril LB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 254 BP; 79 A; 48 C; 63 G; 64 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 41; 135pp; English.
                                                                                                                                                              (UYME-) UNIV MEXICO NACIONAL AUTONOMA. (SILA-) LAB SILANES SA DE CV.
                                                                  26-NOV-2003; 2003US-00721793.
                                                                                                                  02-DEC-2002; 2002US-0430067P.
                                                                                                                                                                                                                                                                                                            WPI; 2005-252753/26.
                                                                                                                                                                                                                                                                                                                                       P-PSDB; ADY85698.
                                                                                                                                                                                                                                 Corona VM, (Possani PLD;
                      24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvention.
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120 180 9 61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA 121 TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT TATITITIGGGTGCTATIGCGAAGGATIGGCCCGAAAGTACACCGACTIGGCCCCTTCCT Gaps ö DB 14; Length 254; 78.3%; Score 150.4; DB 14; Length 86.5%; Pred. No. 8.2e-41; live 0; Mismatches 26; Indels AATAAAAGATGC 192 AATAAATCATGC 192 Best Local Similario, Matches 166; Conservative Local Similarity 61 121 181 181 Query Match 셤 Š 요 ઠે 셤 Š ઠે

181 CCTAATAAAACATGC 195

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ADY85747 standard; DNA; 198 BP.

RESULT 13 ADY85747 (first entry)

02-JUN-2005

ADY85747;

This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a socrpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in correction toxin protein or fragment, hely can be used in compositions or a appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centruroides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stings. This polymucleotide is a DNA sequence encoding the mature protein of a sodium channel modifier toxin isolated from a continue of a sodium channel modifier toxin isolated from a continue of a sodium channel modifier toxin isolated from a continue of a sodium channel modifier toxin isolated from a continue of a sodium channel modifier toxin isolated from a continue of a sodium channel modifier toxin isolated from a continue channel ch 117 120 177 180 Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides. 57 9 scorpion of the Centruroides genus, given in an exemplification of the 58 GAAAACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTAT 118 TGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTT 121 TGCTACGGATTTGGGTGCTATTGTGAAGGATTGTCCGATAGTACACCCGACTTGGCCCCTT 1 AAAGACGGTTATCTGGTGGACAA - - GACGGGCTGCAAATACACTTGCTGGATATTGGGA 1 AAGGAAGGTTATCTGGTGAACAAAAGCACAGGCTGTAAATACAACTGCTTGATATTGGGA Gaps ., , Becerril LB; DB 14; Length 198; gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis. 21; Indels Sequence 198 BP; 67 A; 35 C; 51 G; 45 T; 0 U; 0 Other; Valdez CNA, Score 145.4; DB 14 Pred. No. 3.7e-39; 0; Mismatches 21; (UYME-) UNIV MEXICO NACIONAL AUTONOMA. (SILA-) LAB SILANES SA DE CV. Claim 3; SEQ ID NO 91; 135pp; English. Gurrola BG, 75.7%; 87.7%; 02-DEC-2002; 2002US-0430067P. 26-NOV-2003; 2003US-00721793 178 TCTAATAAAAGATGC 192 Matches 171; Conservative Garcia RMC, WPI; 2005-252753/26. Centruroides noxius. Similarity P-PSDB; ADY85748. US2005065331-A1 Corona VM, ( Possani PLD; 24-MAR-2005 invention Query Match 61 g 셤 ద à à ò ò

122 GAAAACAAAAACTGCGATATGGAATGCAAAGCGAAGAACCAAGGAGGTAGTTACGGCTAT 181

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This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention describes immunogent or antiganic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the generation of antibodies that are able to bind to and neutralize the in vivo effects of scorpion venom. As such, they can be used in compositions to a appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus centruroides. Furthermore, it provides a diagnostic method that uses an immunogenic matrix for the purification of specific immunoglobulins present in a sample that can determine the species of scorpion that has stung an individual through the detection of identifying antibodies. In from scorpion stings. This polynucleotide is a DNA sequence encoding the full length protein of a sodium channel modifier toxin isolated from a succession of the Centruroides genus, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
                                                                                                                                 DNA encoding the full length Mexican scorpion Cn10b toxin protein Seq 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurrola BG, Valdez CNA, Becerril LB;
                                                                                                                                                                       gene; de; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 323 BP; 102 A; 57 C; 80 G; 84 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYME-) UNIV MEXICO NACIONAL AUTONOMA.
(SILA-) LAB SILANES SA DE CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 89; 135pp; English.
                ADY85745 standard; DNA; 323 BP.
                                                                                                                                                                                                                                                                                                                                                            26-NOV-2003; 2003US-00721793.
                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-2002; 2002US-0430067P.
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corona VM, Garcia RMC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-252753/26.
P-PSDB; ADY85746.
                                                                                                                                                                                                                                        Centruroides noxius
                                                                                                                                                                                                                                                                              US2005065331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possani PLD;
                                                                                                02-JUN-2005
                                                                                                                                                                                                                                                                                                                      24-MAR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nvention
                                                        ADY85745;
ADY85745
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This invention relates to novel scorpion toxin polynucleotides and the encoded proteins thereof having any one of 142 fully defined amino acid sequences given in the specification. Specifically, it refers to long chain toxins that block the sodium channels of excitable cells and also short chain toxins that affect Erg type potassium channels. The present invention describes immunogenic or antigenic compositions comprising a scorpion toxin protein or fragment thereof, which can be used for the can experience of scorpion venom. As such, they can be used in compositions or appropriate recombinant fusion proteins in the development of vaccines that can prevent envenomation from stings of scorpions of the genus central recombinant fusion prification of specific immunoglobulins present in a sample that can detection of specific immunoglobulins present in a sample that can detection of identifying antibodies. In addition, it provides methods that are useful for treating envenomation from scorpion stings. This polymuclectide is a DNA sequence encoding the mature protein of a sodium channel modifier toxin isolated from a corpion of the centruroides genus, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated scorpion toxin polypeptide, useful for preventing envenomation from scorpion stings, and as vaccine to prevent envenomation from venom of scorpions of genus Centruroides.
177
                                  241
                118 TGCTACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGAACTTGGCCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Becerril LB;
                                                                                                                                                                                                                                                                                             DNA encoding the scorpion Ce7 toxin mature protein Seq 111.
                                                                                                                                                                                                                                                                                                                               gene; ds; toxin; sodium channel; immunogenicity; antigen; antibody production; venom; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurrola BG, Valdez CNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 111; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYME-) UNIV MEXICO NACIONAL AUTONOMA.
(SILA-) LAB SILANES SA DE CV.
                                                                                                                                                                                           ADY85767 standard; DNA; 189 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-2003; 2003US-00721793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2002; 2002US-0430067P.
                                                                                        242 CCTAATAAAACATGC 256
                                                                        178 TCTAATAAAGATGC 192
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garcia RMC,
                                                                                                                                                                                                                                                                                                                                                                                         Centruroides elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2005-252753/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ADY85768.
                                                                                                                                                                                                                                                                                                                                                                                                                          US2005065331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corona VM, (
Possani PLD;
                                                                                                                                                                                                                                                                02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2005.
                                                                                                                                                                                                                               ADY85767;
                                                                                                                                                             RESULT 15
                                                                                                                                                                               ADY85767
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66.0%; Score 126.8; DB 14; Length 189;

Sequence 189 BP; 55 A; 35 C; 52 G; 47 T; 0 U; 0 Other;

62 AAGGAAGGTTATCTGGTGAACAAAAGCACAGGCTGTAAATACAACTGCTTGATATTGGGA 121 GABARCARATRCTGCARTRGGGARTGCACATGGARGCACCGAGGGGGTARTTACGGCTAT 117

28

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1 AAAGACGGTTATCTGGTGGACAA---GACGGGCTGCAAATACACTTGCTGGATATTGGGA

75.7%; Score 145.4; DB 14; Length 323; 87.7%; Pred. No. 4.5e-39; ive 0; Mismatches 21; Indels 3;

Best Local Similarity 87.7 Matches 171; Conservative

Local Similarity

Query Match

57

Gaps 3;

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6; Gaps
Best Local Similarity 82.8%; Pred. No. 7.9e-33;
Matches 159; Conservative 0; Mismatches 27; Indels
                                                                                   181 AATAAAAGATGC 192
|||||| ||||
178 GATAAAACATGC 189
                         8 8 8 8
                                                                      8 8 8
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Search completed: January 21, 2006, 21:36:21 Job time : 303 secs

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January 21, 2006, 21:28:41; Search time 1730 Seconds (without alignments) 6308.637 Million cell updates/sec
                                                                                                                                                 1 aaagacggttatctggtgga...........ccctttctaataaaagatgc 192
                                                                                                                                                                                                                                         11766282
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              5883141 seqs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 nucleic search, using sw model
                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                        US-10-721-793-115
192
                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: 90 ba:*
2: 90 in:*
3: 90 on:*
3: 90 on:*
3: 90 pat:*
30 pr:*
90 pr:*
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90 pr:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AY351300 Centruroi	AY351297 Centruroi	L05062 Centruroide	AF338460 Centruroi	AY351298 Centruroi	AY351299 Centruroi	AF338448 Centruroi	S81093 Centruroide	AY649868 Centruroi	AY649867 Centruroi		AY351303 Centruroi	AY351301 Centruroi	AY351308 Centruroi	AY351307 Centruroi	L05060 Centruroide	L05061 Centruroide	AY351304 Centruroi
SUMMARIES		ID	AY351300	AY351297	CUDNATOXC	AF338460	AY351298	AY351299	AF338448	S81093	AY649868	AY649867	AY351302	AY351303	AY351301	AY351308	AY351307	CUDNATOXA	CUDNATOXB	AY351304
		DB	5	~	~	~	~	7	~	~	7	~	~	~	7	~	7	N	~	7
		Query Match Length	192	192	319	320	192	192	320	344	258	254	192	192	192	192	192	335	350	192
	de	Query Match	82.5	81.7	81.7	81.7	80.8	80.8	80.8	80.8	79.2	78.3	70.0	70.0	69.2	68.3	66.7	64.9	64.9	64.2
		Score	158.4	156.8	156.8	156.8	155.2	155.2	155.2	155.2	152	150.4	134.4	134.4	132.8	131.2	128	124.6	124.6	123.2
		Result No.	-	7	e	4	Ŋ	9	7	00	σ	10	11	12	13	14	15	16	17	18

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0; Gaps

Query Match 82.5%; Score 158.4; DB 2; Length 192; Best Local Similarity 89.1%; Pred. No. 6.1e-35; Matches 171; Conservative 0; Mismatches 21; Indels 0

ORIGIN

19 123.2 20 123.2 20 121.4 22 121.4 24 121.4 25 121.4 26 119.8 29 119.8 29 119.8 39 119.8 31 118.2 33 118.2 33 118.2 34 118.2 34 113.4 41 113.4 41 113.4 44 113.4 44 113.4 45 102.2 AUTHORS COUGNAL CO	64.2 192 2 AY351306 AY351306 64.1 323 2 AF338453 AF338462 AF338462 AF338462 AF338462	63.2 192 2 AY351305 AY351305 63.2 301 6 AR163001 AR163001 63.2 345 2 CNCM10 Y08270 C 63.2 345 6 AR163005 AR163005	62.4 62.4 322 62.4 322	62.4 323 2 AF338457 AF338457 C 62.4 323 2 AF338458 AF338458 C 61 6 316 2 AF491130 C	61.6 319 2 AF338459 AF338469 61.6 323 2 AF338464 AF8388464 61.7 323 2 AF338464 AF8388464	50.7 2/3 2 AF338454 AF338455 59.9 323 2 AF338455 AF338455	59.1 261 2 AX649861 59.1 314 2 AX649862 50.1 300 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 58.4 316 2 AR491133 AF491133	6 55.0 201 2 A1351310 AY351310 8 54.6 273 2 AY649871 AY649871	ALIGNMENTS	AY351300 192 bp DNA linear INV 31-DEC-2003 Centruroides sculpturatus isolate CsEI beta-toxin gene, partial	cd8. AY351300 AY351300.1 GI:38017458	Centruroides sculpturatus Entruroides sculpturatus Enkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae; Centruroides.	<ol> <li>(bases 1 to 192)</li> <li>Zhu, S.</li> <li>Alignment of beta-toxin nucleotide sequences</li> <li>(Broublished</li> </ol>	2 (bases 1 to 192) Zhu,S.	Direct Submission Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van Evenstraat, Leuven, Flanders 3000, Belgium	sation/Qualifiers	"Centruroides sculpturatus ="genomic DNA" [GBBI" taxon:218467"	<1>192 /product="beta-toxin"	<pre>&lt;1&gt;192 /codon_start=1 /product="beta-toxin" /protein_id="AAR08035.1" /db_xref="G1:3801745x" /translation="xx07x"/xxyxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx</pre>	CYCEGLPDSTQTWPLPNKTC"
								112	22		2		ΣS	•			rce		mRNA	CDS	NISTAC

us-10-721-793-115.rge

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/product="Na+-channel blocking toxin"
/protein_id="AAA28287.1"
/db_xref="G1:304571"
/tb_xref="G1:304571"
FITAGLYUAGYWAKDGYLVDVKGCKKNCYKLGENDYCNR ECKWKHRGGSYGYCYGFGCYCEGLSDSTPTWPLPNKRCGGK"
-1. 56
                                                                                                 CUDNATOXC 319 bp mRNA linear INV 12-AUG-1993 CENTRULOIDER DOXIUS NA+-Channel blocking toxin mRNA, 3' end of cds.
                                                                                                                                                                                                                                                                                                                                        Possani, L.D., Dent, M.A.R., Martin, B.M., Maelicke, A. and Svendsen, I. The amino terminal sequence of several toxins from the venom of the Mexican scorpion Centruroides noxius Hoffmann Carlsberg Res. Commun. 46, 207-214 (1981)
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Carbone, E., Wanke, E., Prestipino, G., Possani, L.D. and Maelicke, A. Selective blockage of voltage-dependent K+ channels by a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning and characterization of cDNAs that code for Na(+)-channel-blocking toxins of the scorpion Centruroides noxius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 (bases 1 to 319)
Vazquez,A., Becerril,B., Martin,B.M., Zamudio,F., Bolivar,F. and Possani,L.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primary structure determination and cloning of the cDNA encoding toxin 4 of the scorpion Centruroides noxius Hoffmann FEBS Lett. 320 (1), 43-46 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           noxius (strain HK9) (library: cDNA to mRNA.
                                                                                                                                                                    L05062.1 GI:304570
Na+ channel; Na+-channel blocking toxin; sodium channel; sodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (sites)
Becerril, B., Vazquez, A., Garcia, C., Corona, M., Bolivar, F. and
Possani, L. D.
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J. Physiol. (Paris) 79 (4), 179-184 (1984)
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/tissue_type="venomous glands"
/dev_stage="adult"
                                                                                                                                                                                                            channel blocking toxin; toxin.
Centruroides noxius (Mexican scorpion)
Centruroides noxius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possani, L.D. Structure of E. Structure of (in) Tu, A.T. (Ed.); HANDBOOK OF NATURAL TOXINS, Vol. 2: Marcel Dekker, Inc., New York (1984)
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lambda gt11) adult venomous glands
Location/Qualifiers
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<1. .260
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Nature 296 (5852), 90-91 (1982)
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/strain="HK9"
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181 AATAAAAGATGC 192
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/codon_start=1
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/db_xref="G1:38017453"
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CYCEGLSDSTPTWPLPNKRC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Centruroides noxius
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
1 (Dases 1 to 192)
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                                                       1 AAGGACGGTTATCTAGTGGAAAAGACGGGCTGCAAAAAGACTTGCTACAAATTGGGAGAA
                                                                                                      AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC
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Submitted (24-JUL-2003) Leuven University,
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="CnGTIV"
/db_xref="taxon:6878"
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product="beta-toxin"
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2 (bases 1 to 192)
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/product="beta-toxin"
/protein id="AAR08033.1"
/db.xref="gg1:38017455"
/translation="ROSTUNDAKGCKKNCYKLGKNDYCNRECRMKHRGGSYGYCYGFG
CYCEGLSDSTPTWPLPNKTC"
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Bvenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
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Centruroides noxius isolate Cnl beta-toxin gene, partial cds.
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Buthida, Buthoidea, Buthidae, Centruroldes.
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      Score 156.8; DB 2;
Pred. No. 1.7e-34;
0; Mismatches 22;
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Pred. No. 5.1e-34;
0; Mismatches 23;
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/mol type="genomic DNA"
/isolate="Cn1"
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/product="beta-toxin"
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/codon_start=1
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Centruroides exilicauda sodium-channel modifier toxin precursor
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1 (Dases 1 to 320, Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. and Possani, L.D. Genes and peptides from the scorpion Centruroides sculpturatus Ewing, that recognize Na(+)-channels
Toxicon 39 (12), 1893-1898 (2001)
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/protein id="AAL23428.1"
/bx xxeE="G1:1644992"
/translation="MNSILMITACLVLIGTVWAKDGYLVEKTGCKKTCYKLGENDFCN
RECKWKHIGGSYGYFYGFGCYCEGLPDSTQTWPLPNKTCGKK"
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251. .253
/note="amidation site"
                                                                                                                             Length 319;
57. .251
/product="Na+-channel blocking toxin"
252. .257
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319
                                                                                                                            Score 156.8; DB 2; Length
Pred. No. 1.7e-34;
0; Mismatches 22; Indels

    .320
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/mol_type="mRNA"
    /db_xref="taxon:6879"
    /country="USA: Tucson, Arizona"
    /note="authority: Bwing"

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Corona, M. and Possani, L.D.
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Centruroides exilicauda
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                                                                                                                             Query Match 81.7%;
Best Local Similarity 88.5%;
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       AATAAAAGATGC 248
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                                                   misc_feature
                 mat_peptide
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AF338460
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                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Evenstraat, Leuven, Planders 3000, Belgium
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="beta-toxin"
/protein id="AAR08034.1"
/db_xref="G1:38017457"
/translation="KESYLVDVKGCKKNCWKLGDNDYCNRECKWKHIGGSYGYCYGFG
CYCEGLPDSTQTWPLPNKTC"
                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae; Centruroides.

1 (bases 1 to 192)
22u, S.
Alignment of beta-toxin nucleotide sequences
                                                                                      AY351299 192 bp DNA linear INV 31-DEC-2003
Centruroides sculpturatus isolate CSE1x beta-toxin gene, partial
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                                                                                                                                                                                                                                                                                                                                                                 sculpturatus"
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                                                                                                                                                                   Centruroides sculpturatus (bark scorpion)
Centruroides sculpturatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.8%; Score 155.2; DB 2
Best Local Similarity 88.0%; Pred. No. 5.1e-34;
Matches 169; Conservative 0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                             /organism="Centruroides
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                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:218467"
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2 (bases 1 to 192)
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                      181 AATAAAACATGC 192
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AATAAAAGATGC
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AY351299.1
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181
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AF338448
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S81093 344 bp mRNA linear INV 24-MAR-2000 Centruroides noxius Na+ channel-specific toxin 1 mRNA, complete
Centruroides exilicauda

Centruroides exilicauda

Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.

Corona, M., Valdez-Cruz, N.A., Merino, B., Zurita, M. and Possani, L.D. Genes and peptides from the scorpion Centruroides sculpturatus

Bwing, that recognize Na(+)-channels

Toxicon 39 (12), 1893-1898 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5. .265
/codon_start=1
/product="sodium-channel modifier toxin precursor CsElx"
/protuch_id="AAL23416.1"
/db_xref="G1:1644968"
/translation="MNSLLMITACLVVIGTVWAKEGYLVDVKGCKKNCWKLGDNDYCN
RRCKWKHIGGSYGYCYGFGCYCEGLPDSTQTWPLPNTTCGKK"
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Submitted (22-JAN-2001) Bioestructura y Reconocimiento Molecular,
Instituto de Biotecnologia, Universidad Nacional Autonoma de
Mexico, Av. Universidad 2001, Cuernavaca, Morelos 62210, Mexico
Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpion
Buthida; Buthoidea; Buthidae; Centruroides.
1 (bases 1 to 344)
Vazquez,A., Tapia,J.V., Eliason,W.K., Martin,B.M., Lebreton,F.,
Delepierre,M., Possani,L.D. and Becerril,B.
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251. .253
/note="amidation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .320
/organism="Centruroides exilicauda"
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/country="USA: Tucson, Arizona"
/note="authority: Ewing"
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Corona, M. and Possani, L.D.
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/translation="KOGYLVRVTGCKKSCYKLGENKFCNRECKMKHRGGSYGYCYFFG
CYCEGLAESTPTWPLPNKSCGKK"
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Centruroides exilicanda Cex9 neurotoxin precursor (Cex9) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
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Institute of Biotechnology UNAM, Av. Universidad 2001, Cuernavaca,
Mor 62250, Mexico
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Valdez-Cruz,N.A., Davila,S., Licea,A., Corona,M., Zamudio,F.Z.,
Garcia-Valdes,J., Boyer,L. and Possani,L.D.
Biochemical, genetic and physiological characterization of venom
components from two species of scorpions: Centruroides exilicanda
Myood and Centruroides sculpturatus Ewing
Biochimie (2004) In press
2 (bases 1 to 254)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.2%; Score 152; DB 2; Length 25 ilarity 87.0%; Pred. No. 4.2e-33; Conservative 0; Mismatches 25; Indels
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                                                                                                           /mol_type="mRNA"
/db_xref="taxon:6879"
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                      Location/Qualifiers
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Centruroides exilicauda
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/gene="Cex10"
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<1. .204
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Mor 62250, Mexico
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="Na+ channel-specific toxin 1"
/protein_id="AAB36085.2"
/db_xref="G1:7322068"
/translation="MNSLLMITACFVLIGTVWAKDGYLVDAKGCKKNCYKLGKNDYCN
RECRMKHRGGSYGYCYGFGCYCEGLSDSTPTWPLPNKTCSGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY649868 258 bp mRNA linear INV 18-AUG-2004 Centruroides exilicauda Cex10 neurotoxin precursor (Cex10) mRNA, partial cds.
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Buthida; Buthoidea; Buthidae; Centruroides.
   Cloning and characterization of the cDNAs encoding Na+
channel-specific toxins 1 and 2 of the scorpion Centruroides noxius
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Submitted (10-JUN-2004) Molecular Medicine and Bioprocesses,
Institute of Biotechnology UNAM, Av. Universidad 2001, Cuernavaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACAAATACTGCAATAGGGAATGCACATGGAAGCACCGAGGAGGTAATTACGGCTATTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AAGGACGGTTATCTGGTCGACGCAAAGGCTGCAAAAAGAATTGCTATAAATTGGGAAAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TACGGATTIGGCTATIGCGAAGGATIGTCCGATAGTACACCGACTIGGCCCCTITCT 180
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Valdez-Cruz,N.A., Davila,S., Licea,A., Corona,M., Zamudio,F.Z., Valdez-Cruz,N.A., Davila,S., Licea,A., Corona,M., Zamudio,F.Z., Garcia-Valdes,J., Boyer,L. and Possani,L.D.
Biochemical, genetic and physiological characterization of venom components from two species of scorpions: Centruroides exilicauda Biochimie (2004) In press
2 (bases 1 to 258)
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                                                                                                                                                                                                                                                                                                                                                                                                                               9. .269 // Apper November 1, Cn1 // Octe="Nat channel-specific toxin 1, Cn1 // Octe="Conceptual translation differs from that in the paper; Cn1 // Octe // Oct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAGACGGTTATCTGGTGGACAAGACGGGCTGCAAATACACTTGCTGGATATTGGGAGAA
                                                                                        Toxicon 33 (9), 1161-1170 (1995)
8585086
GenBank staff at the National Library of Medicine created this entry [NCBI gibbs 175934] from the original journal article.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Na+ channel-specific toxin 1, Cn1"
9. .269
                                                                                                                                                                                                                                                    1. .344
/organism="Centruroides noxius"
                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:6878"
/note="Hoffmann"
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1 AAAGAAGGTTATCTGGTAAACAGCACGGGCTGCAAATACGGTTGCCTGCTATTGGGGAAA
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/mol_type="genomic DNA"
/isolate="CnGTIII"
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/codon_start=1
/product="beta-toxin"
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Matches 156; Conserv
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Direct Submission
Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Bvenstraat, Leuven, Planders 3000, Belgium
Location/Qualifiers
          /codon_start=1
/product="Cex9 neurotoxin precursor"
/protein_id="AAAT98000.1"
/db_xref="G1:51234250"
/translation="MCGYPVEVTGCKKSCYKLGENKFCNRECKWKHRGGSYGYCYFFG
CYCEGLAESTPTWPLPNKSCGKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="beta-toxin"
/protein id="AAR08037.1"
/bx xref="G1:38017463"
/translation="RESYLVNSTGCKYGCLLLGKNEGCDKECKAKNQGGSYGYCYAFG
CWCEGLPESTPTYPLPNKSC"
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Buthida; Buthoidea; Buthidae; Centruroides.

    (bases 1 to 192)

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                                                                                                                                            ö
                                                                                                                  Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 134.4; DB 2; Length 192; larity 81.2%; Pred. No. 5.3e-28; Conservative 0; Mismatches 36; Indels 0
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment of beta-toxin nucleotide sequences Unpublished
                                                                                                                  DB 2;
                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Centruroides noxius"
/mol type="genomic DNA"
/isolate="Cn5"
                                                                                                                 78.3%; Score 150.4; DB 2
86.5%; Pred. No. 1.2e-32;
ive 0; Mismatches 26
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Centruroides noxius
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/codon_start=1
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56; Conservative
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156; Conserv
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AY351303 192 bp DNA linear INV 31-DEC-2003
Centruroides noxius isolate CnGTIII beta-toxin gene, partial cds.
AY351303
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/db_xref="G1:38017465"
/translation="KEGYLVNSTGCKYGCFWLGKNEGCDKECKAKNQGGSYGYCYAFG
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Buthida; Buthoidea; Buthidae; Centruroides.
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                                                                                  61 AACGAAGGCTGCGATAAGGAATGCAAAGCGAAGAACCAAGGAGGTAGTTACGGCTATTGC
                                                                                                                                121 TACGGATTTGGGTGCTATTGCGAAGGATTGTCCGATAGTACACCGACTTGGCCCCTTTCT
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2 (bases 1 to 192)
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Submitted (24-JUL-2003) Leuven University,
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
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llarity 81.2%; Pred. No. 5.3e-28;
Conservative 0; Mismatches 36;
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Centruroides noxius
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<1. . . > 192
/product="beta-toxin"
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AY351307.1 GI:38017472
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/codon_start=1
Unpublished
2 (bases 1 to 192)
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AY351307
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Buthida; Buthoidea; Buthidae; Centruroides.
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CWCEGLPESTPTYPLPNKSC"
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Centruroides noxius isolate Cn10 beta-toxin gene, partial cds.
AY351308
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Buthida; Buthoidea; Buthidae; Centruroides.
1 (bases 1 to 192)
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Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
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                                                   AY351301 192 bp DNA linear INV 31-DEC-2003
Centruroides sculpturatus isolate CsEv2a beta-toxin gene, partial
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80.7%; Pred. No. 1.5e-27;
ive 0; Mismatches 37;
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Centruroides sculpturatus
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Centruroides noxius
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/codon start=1
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Best Local Similarity 80.79
Matches 155; Conservative
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Zhu,S.
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AY351308
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Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Butholdea; Buthidae; Centruroldes.
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Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, B van
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
Direct Submission
Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
1. :192
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/mol type="Centrucoides noxius"
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/d_xref="G1:38017475"
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CWCEGLPESTPTYPIPGKTC"
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Centruroides sculpturatus isolate CsEvld beta-toxin gene, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.3%; Score 131.2; DB 2; Length 80.2%; Pred. No. 4.4e-27; ative 0; Mismatches 38; Indels
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|organism="Centruroides sculpturatus"
|mol type="genomic DNA"
|isolate="CsEvid"
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Centruroides sculpturatus
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                                                                                                                                     Query Match 66.7%; Score 128; DB 2; Length 192; Best Local Similarity 79.2%; Pred. No. 3.7e-26; Matches 152; Conservative 0; Mismatches 40; Indels
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Search completed: January 21, 2006, 22:05:18 Job time : 1731 secs

## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases: older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_Main) and .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

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